

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:10:02 ; Search time 15.1966 seconds
(without alignments)
118.029 Million cell updates/sec

Title: US-10-089-500-3

Perfect score: 28

Sequence: 1 HYAMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq_23sep04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003s:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	5	4	AAB81979
2	28	100.0	5	6	ABU11004
3	28	100.0	119	3	AAB14979
4	28	100.0	119	4	AAB81985
5	28	100.0	119	4	AAB81989
6	28	100.0	119	6	ABU11012
7	28	100.0	119	6	ABU11010
8	28	100.0	119	6	ABR83239
9	28	100.0	119	6	ABR83238
10	28	100.0	119	6	ABU16272
11	28	100.0	119	6	ABU43645
12	28	100.0	119	6	ABM71799
13	28	100.0	130	2	AAR33256
14	28	100.0	130	2	AAR53341
15	28	100.0	130	2	AAV28369
16	28	100.0	130	3	AAB01627
17	28	100.0	138	4	AAB81977
18	28	100.0	138	6	ABU11002
19	28	100.0	156	4	ABG28979
20	28	100.0	280	4	AA896839
21	28	100.0	280	8	ADN46873
22	28	100.0	514	7	ABO71592
23	28	100.0	582	4	AAB81987
24	28	100.0	582	4	AAB81991
25	28	100.0	1268	4	AAW79111

26	28	100.0	1270	4	AA880095	AA880095 Human pro
27	28	100.0	1669	4	ABB63980	ABB63980 Drosophila
28	28	100.0	14	4	AA897232	AA897232 Human pep
29	25	89.3	50	3	AA834620	AA834620 Human sec
30	25	89.3	76	4	AA003185	AA003185 Human pol
31	25	89.3	108	4	AA003855	AA003855 Human pol
32	25	89.3	113	6	AD807666	AD807666 Human pol
33	25	89.3	116	4	AA881907	AA881907 S. epider
34	25	89.3	126	6	ABU49557	ABU49557 Protein e
35	25	89.3	133	6	AD807674	AD807674 Altolococ
36	25	89.3	134	6	AD807668	AD807668 Altolococ
37	25	89.3	146	4	AA002622	AA002622 Human pol
38	25	89.3	150	4	AAU17373	AAU17373 Novel sig
39	25	89.3	150	7	ADB94081	ADB94081 Human nov
40	25	89.3	164	4	ABG21786	ABG21786 Novel hum
41	25	89.3	180	5	AA666027	AA666027 Ryk prote
42	25	89.3	181	5	AA666026	AA666026 Ryk prote
43	25	89.3	191	5	AA666025	AA666025 Ryk prote
44	25	89.3	204	5	AA666034	AA666034 Human Ryk
45	25	89.3	214	6	ADB10122	ADB10122 Altolococ

ALIGNMENTS

RESULT 1
AAB81979
ID AAB81979 standard; peptide; 5 AA.
AC AAB81979;
DT 03-JUL-2001 (first entry)
XX Ganglioside GD3 specific antibody related peptide SEQ ID NO: 3.
DE Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KM cancer.
XX Mus musculus.
XX WO200123432-A1.
XX PN
XX PD
XX 05-APR-2001.
XX PF 29-SEP-2000; 2000WO-JP006774.
XX PR 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX DR
XX PT New human type complementation-determining region-transplanted antibody
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX PT
XX Claim 5; Page 141; 183pp; Japanese.
XX PS
XX The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumors, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX SO Sequence 5 AA;
Query Match 100.0%; Score 28; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 1 HYAMS 5

RESULT 2

ABU1004 standard; peptide; 5 AA.

ABU1004;

04-FEB-2003 (first entry)

Modified ganglioside GD3 antibody associated peptide #1.

Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

Mus musculus.

WO200278739-A1.

10-OCT-2002.

29-MAR-2002; 2002WO-JP0031170.

29-MAR-2001; 2001JP-00097483.

(KYOW) KYOWA HAKKO KOGYO KK.

Shitara K, Niwa R, Kanazawa J, Asada M;

WPI; 2003-067410/06.

Drugs containing genetically-modified antibody against ganglioside GD3, its fragment, immunocompetent cell activators or/and antitumor agents in combination, applicable in treating malignant tumor like melanoma.

Claim 6; Page 98; 121pp; Japanese.

The invention describes drugs contain a genetically-modified antibody against ganglioside GD3 or its fragment and at least 1 of a substance capable of activating immunocompetent cells and a substance having an antitumor activity in combination. The drugs can be used to treat tumour like melanoma and can provide a treatment with enhanced therapeutic effect and little side-reactions, particularly to relieve problems of side-effects during the conventional single administration. This sequence represents a peptide associated with the anti- ganglioside GD3 antibody

Sequence 5 AA;

Query Match 100.0%; Score 28; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 1 HYAMS 5

RESULT 3
AAB14979
ID AAB14979 standard; protein; 119 AA.

AAB14979;

01-DEC-2000 (first entry)

Staphylococcus aureus phosphopantetheinyl transferase protein AcpS.

AcpS; phosphopantetheinyl transferase; antibacterial;
Helicobacter pylori; stomach cancer; ulcer; gastritis.

OS Staphylococcus aureus.

WO200040594-A1.

13-JUL-2000.

13-DEC-1999; 99WO-US029464.

08-JAN-1999; 99US-00227700.

(SMIK) SMITHKLINE BEECHAM CORP.

Pearson SC;

WPI; 2000-465946/40.

N-PSDB; AAA73679.

New isolated Staphylococcus aureus polypeptide, referred to as AcpS, for treating or diagnosing individuals with a disease in need of enhanced or inhibited activity or expression of the polypeptide.

Claim 1; Page 3; 38pp; English.

The present sequence is the Staphylococcus aureus phosphopantetheinyl transferase family protein AcpS. The DNA encoding this sequence was isolated from a Staphylococcus aureus DNA library. The AcpS protein and its agonists, antagonists or nucleic acids may be used to treat individuals that are in need of enhanced or inhibited activity or expression of the protein, or an immunological response to it. They may also be used to detect and treat microbial diseases, such as Helicobacter pylori infections that cause stomach cancer, ulcers and gastritis

Sequence 119 AA;

Query Match 100.0%; Score 28; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 106 HYAMS 110

RESULT 4
AAB81985
ID AAB81985 standard; protein; 119 AA.

AAB81985;

03-JUL-2001 (first entry)

Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.

Ganglioside; GD3; complementarity determining region; CDR; antibody;

cancer.

Synthetic.

WO200123432-A1.

05-APR-2001.

29-SEP-2000; 2000WO-JP006774.

30-SEP-1999; 99JP-00278291.

06-APR-2000; 2000JP-00105088.

(KYOW) KYOWA HAKKO KOGYO KK.

Hanai N, Shitara K, Nakamura K, Niwa R;
WPI; 2001-266143/27.

PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.

PS Claim 20; Page 142-143; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX Sequence 119 AA;

Query Match 100.0%; Score 28; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 31 HYAMS 35

RESULT 5
AAB81989
ID AAB81989 standard; protein; 119 AA.

XX AAB81989;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.

KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.

OS Mus musculus.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI; 2001-266143/27.

PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.

PS Claim 10; Page 173-174; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX Sequence 119 AA;

Query Match 100.0%; Score 28; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 31 HYAMS 35

RESULT 6
ABU11012
ID ABU11012 standard; protein; 119 AA.

XX ABU11012;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #5.

KM Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

OS Mus musculus.

PN WO200278739-A1.

PD 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Shitara K, Niwa R, Kanazawa J, Asada M;

DR WPI; 2003-067410/06.

PT Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.

PS Claim 7; Page 112-113; 121pp; Japanese.

CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 119 AA;

Query Match 100.0%; Score 28; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 31 HYAMS 35

RESULT 7
ABU11010
ID ABU11010 standard; protein; 119 AA.

XX ABU11010;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #3.

KM Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

OS Synthetic.

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PN WO200278739-A1.
XX
XX 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-JP003170.
XX
XX 29-MAR-2001; 2001JP-00097483.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Niwa R, Kanazawa J, Asada M;
XX MPI; 2003-067410/06.
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX
XX Claim 8; Page 99; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumour
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 119 AA;
XX
XX Query Match 100.0%; Score 28; DB 6; Length 119;
XX Best Local Similarity 100.0%; Pred. No. 79;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HYAMS 5
XX 31 HYAMS 35
XX
XX Db
XX
XX RESULT 8
XX ABR83239
XX ID ABR83239 standard; protein; 119 AA.
XX
XX AC ABR83239;
XX
XX 30-SEP-2003 (first entry)
XX
XX S. aureus acyl carrier protein synthase acps protein SEQ ID NO:34.
XX
XX Crystallised recombinant polypeptide; Staphylococcus aureus; vaccine;
XX Streptococcus pneumoniae; Helicobacter pylori; Pseudomonas aeruginosa;
XX membrane biosynthesis; crystal form; antibacterial; crystal structure;
XX immunological response; vaccination; ftsz; fabz; fabG; acps; murD; murC;
XX fabH; tagD; obg.
XX
XX Staphylococcus aureus.
XX
XX WO2003027139-A2.
XX
XX 03-APR-2003.
XX
XX 24-SEP-2002; 2002WO-CA001443.
XX
XX 24-SEP-2001; 2001US-0324449P.
XX
XX 01-OCT-2001; 2001US-0324504P.
XX
XX 03-OCT-2001; 2001US-0326269P.
XX
XX 24-OCT-2001; 2001US-0339560P.
XX
XX 25-OCT-2001; 2001US-0337471P.
XX
XX 26-OCT-2001; 2001US-0340002P.
XX
XX 26-OCT-2001; 2001US-0340002P.
XX
XX 26-OCT-2001; 2001US-0340027P.
XX

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PR 18-DEC-2001; 2001US-0341767P.
PR 21-DEC-2001; 2001US-0344307P.
PR 27-DEC-2001; 2001US-0343946P.
XX
XX (AFFI-) AFFINIUM PHARM INC.
XX
XX Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;
XX Canadien V, Domagala M, Houston S, Kanagarajah D, Li Q, Mangoury K;
XX McDonald M, Necakov S, Ng I, Pinder B, Sheldrick B, Vallee F;
XX Viola C, Wrezel O;
XX
XX MPI; 2003-441048/41.
XX
XX N-PSDB; ACF06198.
XX
XX Novel crystallized recombinant polypeptides from Staphylococcus aureus,
XX Streptococcus pneumoniae and Helicobacter pylori and which are involved
XX in membrane biosynthesis, useful as targets for pathogenic bacteria.
XX
XX Claim 84; Fig 29; 312pp; English.
XX
XX The present invention describes a crystallised recombinant polypeptide
XX (1) comprising amino acid sequence of polypeptides from Staphylococcus
XX aureus, Streptococcus pneumoniae, Helicobacter pylori and Pseudomonas
XX aeruginosa and which are involved in membrane biosynthesis, or amino acid
XX sequences having at least 90 % identity with the polypeptide sequence,
XX where the polypeptide is in crystal form. (1) has antibacterial activity
XX and can be used in vaccines. (1) is useful for designing a modulator for
XX the prevention or treatment of S. aureus, H. pylori, S. pneumoniae, and
XX P. aeruginosa-related disease or disorder. (1) is also useful for
XX identifying small molecules that bind to a recombinant polypeptide. The
XX structural and functional information of (1) aid in the discovery and
XX design of therapeutic and diagnostic molecules. The crystal structure is
XX useful to make a structural or computer model of the polypeptide, complex
XX or its portion. (1) can be used for inducing an immunological response in
XX an individual and as an antigen for vaccination of a host to produce
XX specific antibodies which protect against invasion of bacteria, for
XX example by blocking adherence of bacteria to damaged tissue. ACF06195 to
XX ACF06232 and ABR83203 to ABR83333 represent sequences used in the
XX exemplification of the present invention
XX
XX Sequence 119 AA;
XX
XX Query Match 100.0%; Score 28; DB 6; Length 119;
XX Best Local Similarity 100.0%; Pred. No. 79;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HYAMS 5
XX 106 HYAMS 110
XX
XX Db
XX
XX RESULT 9
XX ABR83238
XX ID ABR83238 standard; protein; 119 AA.
XX
XX AC ABR83238;
XX
XX 30-SEP-2003 (first entry)
XX
XX S. aureus acyl carrier protein synthase acps protein SEQ ID NO:32.
XX
XX Crystallised recombinant polypeptide; Staphylococcus aureus; vaccine;
XX Streptococcus pneumoniae; Helicobacter pylori; Pseudomonas aeruginosa;
XX membrane biosynthesis; crystal form; antibacterial; crystal structure;
XX immunological response; vaccination; ftsz; fabz; fabG; acps; murD; murC;
XX fabH; tagD; obg.
XX
XX Staphylococcus aureus.
XX
XX WO2003027139-A2.
XX
XX 03-APR-2003.
XX

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ABU43645
 ID ABU43645 standard; protein; 119 AA.
 XX
 AC ABU43645;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #29172.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Staphylococcus haemolyticus.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 XX
 PR 06-SEP-2001; 2001US-00948993.
 XX
 PR 25-OCT-2001; 2001US-0342923P.
 XX
 PR 08-FEB-2002; 2002US-00072851.
 XX
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 XX
 DR N-PSDB; ACA47515.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 Claim 25; SEQ ID NO 71569; 1766bp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 119 AA:

Query Match 100.0%; Score 28; DB 6; Length 119;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
 |||||
 Db 107 HYAMS 111

RESULT 12
 ABM71799
 ID ABM71799 standard; protein; 119 AA.
 XX
 AC ABM71799;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Staphylococcus aureus protein #1039.
 XX
 KM Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KM enzymatic assay; antibiotic target.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200294868-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 27-MAR-2002; 2002WO-IB002637.
 XX
 PR 27-MAR-2001; 2001GB-00007661.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Masignani V, Mora M, Scarselli M;
 XX
 DR WPI; 2003-120786/11.
 XX
 DR N-PSDB; ACF73359.
 XX
 PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.
 XX
 PS Claim 1; SEQ ID NO 2078; 499p; English.

The invention relates to novel genes and encoded proteins from *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to *Staphylococcus bacteria*, specifically an infection caused by *S. aureus*. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel *S. aureus* proteins of the invention

Sequence 119 AA:

Query Match 100.0%; Score 28; DB 6; Length 119;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
 |||||
 Db 106 HYAMS 110

RESULT 13
 AAR33256
 ID AAR33256 standard; protein; 130 AA.
 XX
 AC AAR33256;
 XX

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DT 25-MAR-2003 (revised)
DT 12-JUL-1993 (first entry)
XX
XX
DE Rat immunoglobulin H chain variable region of pKM641HA3.
XX
XX Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
XX humanised; chimeric; antibody; expression vector.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT Protein /note= "Signal peptide"
FT Protein 11..130
FT Protein /note= "Mature protein"
XX
XX EP533199-A2.
XX
XX 24-MAR-1993.
XX
XX 18-SEP-1992; 92EP-00116026.
XX
XX 18-SEP-1991; 91UP-00238375.
XX
XX (KYOW ) KYOWA HAKKO KOGYO CO LTD.
XX
XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX WPI; 1993-095510/12.
XX DR N-PSDB; AAQ33257.
XX
XX Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
XX cancers, such as melanoma, neuroblastoma, etc.
XX
XX Claim 6; Page 29-30; 63pp; English.
XX
XX The sequences given in AAR33256-57 represent rat heavy and light chain
XX variable regions respectively. The DNA sequences encoding these proteins
XX were used in the construction of humanised chimeric antibody expression
XX vectors. In these humanised antibodies none of the amino acids of the non
XX -human animal Ab variable region have been changed. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
SQ Sequence 130 AA;

Query Match 100.0%; Score 28; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
Db 41 HYAMS 45

RESULT 14
AAR53341
ID AAR53341 standard; protein; 130 AA.
XX
XX AAR53341;
XX
XX 18-NOV-1994 (first entry)
XX
XX KM641 L chain variable region.
XX
XX Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
XX expression vector; heavy; light; chain; hypervariable region; CDR;
XX constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..10
XX /label= sig_peptide
XX

```

```

XX
XX AU9346181-A.
XX
XX 17-MAR-1994.
XX
XX 07-SEP-1993; 93AU-00046181.
XX
XX 07-SEP-1992; 92UP-00238452.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
XX WPI; 1994-126857/16.
XX DR N-PSDB; AAQ45439.
XX
XX Humanised antibody specific for ganglioside GM2 - used for producing a
XX cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX
XX Example 2; Page 116-117; 191pp; English.
XX
XX Example 2 describes the construction of the vector pCh1641HA1 for
XX chimeric human antibody H chain expression. mRNA from mouse anti-GD3
XX monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
XX cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
XX chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
XX AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
XX was constructed by joining the H chain variable region gene from
XX pKM641HA3 to a vector for chimeric human Ab H chain expression using the
XX synthetic DNAs given in AAQ63439 and AAQ63440
XX
SQ Sequence 130 AA;

Query Match 100.0%; Score 28; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
Db 41 HYAMS 45

RESULT 15
AAY28369
ID AAY28369 standard; protein; 130 AA.
XX
XX AAY28369;
XX
XX 04-NOV-1999 (first entry)
XX
XX pKM641 HA3 immunoglobulin heavy chain.
XX
XX antibody; nucleotide; genomic; hypervariable region; chimeric;
XX light chain; amino acid.
XX
XX Mus sp.
XX
XX US5939532-A.
XX
XX 17-AUG-1999.
XX
XX 07-JUN-1995; 95US-00483528.
XX
XX 07-SEP-1993; 93US-00116778.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
XX WPI; 1999-468416/39.
XX DR N-PSDB; AAY99462.
XX
XX Chimeric human antibody expression vectors.
XX

```

XX Example 1; Col 99-101; 188bp; English.
 CC This immunoglobulin region was isolated from pKM641H3. This sequence has
 CC no methionine initiation codon and the leader sequence was partly
 CC lacking. The chimeric human antibodies are useful in the treatment of
 CC cancer, especially that which is of neural ectodermal origin. In contrast
 CC to prior art constructs based on mouse monoclonal antibodies, the
 CC chimeric human antibodies do not cause anti-mouse immunoglobulin
 CC production. The chimeric human antibodies have a prolonged half-life and
 CC a reduced frequency of adverse effects when compared to mouse monoclonal
 CC antibodies
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 28; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYAMS 5
 DB 41 HYAMS 45
 RESULT 16
 AAB01627
 ID AAB01627 standard; protein; 130 AA.
 XX
 AC AAB01627;
 XX
 DT 07-DEC-2000 (first entry)
 XX
 DE Murine immunoglobulin heavy chain variable region.
 XX
 KM Mouse; immunoglobulin; H chain; heavy chain; variable region; cancer;
 KM humanised antibody.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..10
 FT /label= signal_peptide
 FT 11..130
 FT Protein /label= mature_immunoglobulin_heavy_chain_variable region
 PN EP1013761-A2.
 PD 28-JUN-2000.
 XX
 PF 18-SEP-1992; 99EP-00124345.
 XX
 PR 18-SEP-1991; 91UP-00238375.
 PR 18-SEP-1992; 92EP-00116026.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
 PI WPI; 2000-402204/35.
 DR N-PSDB; AAA51003.
 XX
 PT New humanized chimera antibody KM-871 useful for treating cancer,
 PT comprises variable region of mouse monoclonal antibody, reactive with
 PT ganglioside and human antibody constant region.
 XX
 PS Claim 14; Page 27-28; 65pp; English.
 XX
 CC The present sequence is a murine immunoglobulin heavy chain variable
 CC region from plasmid KM-641. The coding sequence was used in the creation
 CC of an expression vector, along with the sequence for a human antibody, to
 CC produce humanised chimaeric antibodies, which can be used to treat
 CC cancer. Humanised chimaeric antibodies are more effective than mouse
 CC antibodies as they do not provoke a reaction in the human and side

CC effects, such as the formation of anti-mouse immunoglobulin antibody and
 CC the rapid half-life of the immunoglobulins, do not occur
 XX
 SQ Sequence 138 AA;
 Query Match 100.0%; Score 28; DB 3; Length 130;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYAMS 5
 DB 41 HYAMS 45
 RESULT 17
 AAB81977
 ID AAB81977 standard; protein; 138 AA.
 XX
 AC AAB81977;
 XX
 DT 03-JUL-2001 (first entry)
 XX
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.
 XX
 KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
 KM cancer.
 OS Mus musculus.
 XX
 PN WO200123432-A1.
 PD 05-APR-2001.
 XX
 PF 29-SEP-2000; 2000WO-JP006774.
 XX
 PR 30-SEP-1999; 99JP-00278291.
 PR 06-APR-2000; 2000JP-00105088.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Hanai N, Shitara K, Nakamura K, Niwa R;
 PI WPI; 2001-266143/27.
 DR
 XX
 XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 PS Example 1; Page 138-139; 183pp; Japanese.
 XX
 CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 XX
 SQ Sequence 138 AA;
 Query Match 100.0%; Score 28; DB 4; Length 138;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYAMS 5
 DB 50 HYAMS 54
 RESULT 18
 ABU11002
 ID ABU11002 standard; protein; 138 AA.
 XX
 AC ABU11002;

```

XX 04-FEB-2003 (first entry)
XX Modified ganglioside GD3 antibody associated protein #1.
XX
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
XX Mus musculus.
XX WO200278739-A1.
XX
XX 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-JP003170.
XX
XX 29-MAR-2001; 2001JP-00097483.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Niwa R, Kanazawa J, Asada M;
XX WPI; 2003-067410/06.
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX
XX Example 3; Page 97; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumour
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 138 AA;
SQ
Query Match 100.0%; Score 28; DB 6; Length 138;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
DB 50 HYAMS 54

```

RESULT 19
ABG28979
ID ABG28979 standard; protein; 156 AA.
XX
AC ABG28979;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #28970.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX

```

PA (HYSS-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS93166.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 59338; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 156 AA;
SQ
Query Match 100.0%; Score 28; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
DB 49 HYAMS 53

```

RESULT 20
AAB96839
ID AAB96839 standard; protein; 280 AA.
XX
AC AAB96839;
XX
DT 29-OCT-2001 (first entry)
XX
DE Putative P. abyssal periplasmic serine protease.
XX
XX Hyperthermophilic archaeon; hyperthermophilic protein.
XX
XX Pyrococcus abyssi.
XX
XX FR2792651-A1.
XX
XX 27-OCT-2000.
XX
XX 21-APR-1999; 99FR-00005034.
XX
XX 21-APR-1999; 99FR-00005034.
XX
XX (CNRS) CNRS CENT NAT RECH SCI.
XX (IFRE-) IFREMER INST FR RECH EXPL MER.
XX Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;

PI Querellou J, Weissenbach J, Saurin W, Hellig R;
XX WPI; 2001-126236/14.
XX
XX New nucleotide sequences isolated from *Pyrococcus abyssi* encode proteins
PT useful in industry.
PS
XX Claim 7, Page 1634; 1657pp; French.
XX
XX The present invention relates to the genomic sequence of *Pyrococcus*
CC *abyssi* (see AAF86431 and AAH41223-7) and *P. abyssi* proteins. *P. abyssi* is
CC a hyperthermophilic archaeon, which is isolated from deep-sea
CC hydrothermal vents. The present sequence is one such *P. abyssi* protein.
CC The proteins of the present invention have various potential industrial
CC uses, since the proteins are stable at very high temperatures, some up to
CC 110 degrees centigrade. Note: This patent is in the same patent family as
CC WO2000065062, which contains additional sequences as shown in AAB99132-
CC AAB99143, AAH75903-AAH75920 and AAG66436
XX
SQ Sequence 280 AA;

Query Match 100.0%; Score 28; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 126 HYAMS 130

RESULT 21
ADN46873
ID ADN46873 standard; protein; 280 AA.
XX
AC ADN46873;
XX
DT 01-JUL-2004 (first entry)
XX
DE *Thermococcus kodakaraensis* KOD1 protein sequence SeqID751.
XX
XX Gene disruption; gene targeting; marker gene; transformation;
KM homologous recombination; hyperthermostable archaeobacterium; KOD1,
KM gene structure; gene function; enzyme activity; medicine;
KM forensic science; food; drug inspection; molecular biology; immunology.
XX
OS *Thermococcus kodakaraensis*.
XX
PN WO2004022736-A1.
XX
PD 18-MAR-2004.
XX
PF 29-AUG-2003; 2003WO-IB003597.
XX
PR 30-AUG-2002; 2002JP-00319011.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PI Imanaka T, Atomi H;
XX
XX WPI; 2004-257583/24.
XX
PT Method for disrupting targeted gene in genome of organism particularly
PT thermostable bacterium and with genome chips for analysis, applicable in
PT studying gene structure and functions.
XX
PS Claim 9; SEQ ID NO 751; 598bp; Japanese.
XX
XX This invention relates to a novel method for targeting disruption of an
CC arbitrary gene in a genome of an organism which comprises providing the
CC whole sequential data of the genome of such organism, selecting at least
CC 1 arbitrary region in the sequence, providing a vector that contains a
CC sequence homologous with the selected region and a marker gene,
CC transformation, and homologous recombination. The genome is preferably

CC the genome of a hyperthermostable archaeobacterium, particularly
CC *Thermococcus kodakaraensis* KOD1. The method is for targeting the
CC disruption of a gene in the genome of an organism, which is applicable in
CC studying gene structure and functions as well as enzyme activities of
CC encoded proteins and useful in medicine, forensic science, food or drug
CC inspection, molecular biology and immunology. With this method, the
CC disruption of a gene at an arbitrary position in a genome can be achieved
CC efficiently and reliably. The present sequence is that of a protein
CC encoded by the genome of *Thermococcus kodakaraensis* which was derived
CC using the method of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 280 AA;

Query Match 100.0%; Score 28; DB 8; Length 280;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 126 HYAMS 130

RESULT 22
ABO71592
ID ABO71592 standard; protein; 514 AA.
XX
XX ABO71592;
AC
XX
DT 29-JUL-2004 (first entry)
XX
DE *Pseudomonas aeruginosa* polypeptide #3767.
XX
XX *Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.*
XX
OS *Pseudomonas aeruginosa*.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
XX
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
XX WPI; 2003-615309/58.
XX
DR N-PSDB; ABD05163.
XX
PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 20338; 455bp; English.
XX
XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-*P. aeruginosa* drugs, as templates for recombinant
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
CC infection, and in detection of *P. aeruginosa* sequences or other sequences
CC of *Pseudomonas* species using biochip technology. Sequences ABO67826-

CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html

XX
SQ Sequence 514 AA;

Query Match 100.0%; Score 28; DB 7; Length 514;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
DB 362 HYAMS 366

RESULT 23

AAAB81987
ID AAB81987 standard; protein; 582 AA.

XX
AC AAB81987;

XX
DT 03-JUL-2001 (first entry)

XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.

XX
KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
cancer.

XX
OS Synthetic.

XX
PN WO200123432-A1.

XX
PD 05-APR-2001.

XX
PF 29-SEP-2000; 2000WO-JP006774.

XX
PR 30-SEP-1999; 99JP-00278291.

XX
PR 06-APR-2000; 2000JP-00105088.

XX
PA (KYOW) KYOWA HAKKO KOGYO KK.

XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX
DR WPI; 2001-266143/27.

XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors; with low antigenicity, little side effects but potent
PT activity in cancer.

XX
PS Claim 41; Page 168-172; 183pp; Japanese.

XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX
SQ Sequence 582 AA;

Query Match 100.0%; Score 28; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
DB 31 HYAMS 35

RESULT 24

AAAB81991
ID AAB81991 standard; protein; 582 AA.

XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)

XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.

XX
KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
cancer.

XX
OS Synthetic.

XX
PN WO200123432-A1.

XX
PD 05-APR-2001.

XX
PF 29-SEP-2000; 2000WO-JP006774.

XX
PR 30-SEP-1999; 99JP-00278291.

XX
PR 06-APR-2000; 2000JP-00105088.

XX
PA (KYOW) KYOWA HAKKO KOGYO KK.

XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX
DR WPI; 2001-266143/27.

XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors; with low antigenicity, little side effects but potent
PT activity in cancer.

XX
PS Claim 39; Page 175-179; 183pp; Japanese.

XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX
SQ Sequence 582 AA;

Query Match 100.0%; Score 28; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
DB 31 HYAMS 35

RESULT 25

AAAM79111
ID AAM79111 standard; protein; 1268 AA.

XX
AC AAM79111;

XX
DT 06-NOV-2001 (first entry)

XX
DE Human protein SEQ ID NO 1773.

XX
KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorder; arthritis; inflammation.

XX
OS Homo sapiens.

XX
PN WO200157190-A2.

XX
PD 09-AUG-2001.

XX
PF 05-FEB-2001; 2001WO-US004098.

XX 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSSEQ INC.
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR N-PSDB; AAKS2244.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 20; Page 4124-4126; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 1268 AA;
XX
QY Query Match 100.0%; Score 28; DB 4; Length 1268;
DB Best Local Similarity 100.0%; Pred. No. 1.1e+03; Mematches 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
DB 182 HYAMS 186
XX
RESULT 26
AAM80095
ID AAM80095 standard; protein; 1270 AA.
XX
AC AAM80095;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3741.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PR 05-FEB-2001; 2001WO-US004098.
XX
PF 03-FEB-2000; 2000US-00496914.
XX

PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSSEQ INC.
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR N-PSDB; AAKS3228.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 20; Page 422-423; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 1270 AA;
XX
QY Query Match 100.0%; Score 28; DB 4; Length 1270;
DB Best Local Similarity 100.0%; Pred. No. 1.1e+03; Mematches 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
DB 182 HYAMS 186
XX
RESULT 27
ABB63980
ID ABB63980 standard; protein; 1669 AA.
XX
AC ABB63980;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 18732.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX

PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL08083.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 18732; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
 CC sequences (ABU1840-ABU15175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1669 AA;

Query Match 100.0%; Score 28; DB 4; Length 1669;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
 |||||
 DB 566 HYAMS 570

RESULT 28
 ID AAM97232 standard; peptide; 14 AA.
 XX
 AC AAM97232;

XX
 XX 24-JAN-2002 (first entry)

XX Human peptide #507 encoded by a SNP oligonucleotide.
 DE
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cyostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.

XX Homo sapiens.
 OS
 XX WO200147944-A2.
 PN
 XX 05-JUL-2001.
 PD
 XX 28-DEC-2000; 2000WO-US035498.
 PF
 XX 28-DEC-1999; 99US-0173419P.
 PR 27-DEC-2000; 2000US-00173419.
 XX

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.
 XX

PS Disclosure; Page 3779; 4143pp; English.
 XX
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukemia), diseases of the nervous
 CC system and an infection of pathogenic organisms
 XX

Query Match 89.3%; Score 25; DB 4; Length 14;
 Best Local Similarity 80.0%; Pred. No. 39;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
 |||||
 DB 1 HYAMS 5

RESULT 29
 ID AAB34620 standard; protein; 50 AA.
 XX
 AC AAB34620;

XX
 XX 26-JAN-2001 (first entry)

DE Human secreted protein sequence encoded by gene 44 SEQ ID NO:104.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
 KW antineumatic; antiproliferative; cyostatic; cardiant; vasotrophic;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; vitruclide;
 KW fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
 KW hyperproliferative disorder; cancer; cardiovascular disorder; infection;
 KW cerebrovascular disorder; angiogenesis; nervous system disorder;
 KW ocular disorder; wound healing; skin aging; food additive; preservative.

XX Homo sapiens.
 OS
 XX WO200056751-A1.

PN 28-SEP-2000.

PD 09-MAR-2000; 2000WO-US006013.

PF 19-MAR-1999; 99US-0125360P.

PR 11-JUN-1999; 99US-0138626P.

PR 03-DEC-1999; 99US-0168662P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-579482/54.

XX N-PSDB; AAC59781.

XX Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 PT Claim 11; Page 387; 419pp; English.

XX The polynucleotide sequences given in AAC59738 to AAC59787 encode the

CC human secreted proteins given in AAB34577 to AAB34676. AAB34677 to
CC AAB34686 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Example of activities include:
CC antihypertic; immunosuppressive; antirheumatic; antiproliferative;
CC cytostatic; caudant; vasotropic; cerebroprotective; nootropic;
CC neuroprotective; antibacterial; virucide; fungicide; and
CC ophthalmological. The polynucleotides and proteins can be are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases, hyperproliferative disorders e.g. neoplasms and
CC cancers of the breast or liver, cardiovascular disorders, cerebrovascular
CC disorders, angiodenesis, nervous system disorders, infections caused by
CC bacteria, viruses and fungi and ocular disorders. The proteins can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The proteins can also be used as a
CC food additive or preservative to increase or decrease storage
CC capabilities. AAC59729 to AAC59737 and AAB34576 represent sequences used
CC in the exemplification of the present invention
XX

SQ Sequence 50 AA;

Query Match 89.3%; Score 25; DB 3; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HVAMS 5
|||:
36 HYAMT 40

RESULT 30
AAO03185
ID AAO03185 standard; protein; 76 AA.
XX

AAO03185;

06-NOV-2001 (first entry)

Human polypeptide SEQ ID NO 17077.

Human: cytokine; cell proliferation; cell differentiation; gene therapy;

tissue growth factor; stem cell growth factor; haematopoiesis;

nervous system disorders; arthritis; inflammation.

Homo sapiens.

MO200164835-A2.

26-FEB-2001; 2001MO-US004927.

28-FEB-2000; 2000US-00515126.

18-MAY-2000; 2000US-00577409.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-514838/56.

N-PSDB; AAI83116.

Isolated nucleic acids and polypeptides, useful for preventing diagnosing
and treating e.g. leukemia, inflammation and immune disorders.

Claim 20; SEQ ID NO 17077; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 76 AA;

Query Match 89.3%; Score 25; DB 4; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HVAMS 5
|||:
5 HYAMT 9

RESULT 31
AAO03855
ID AAO03855 standard; protein; 108 AA.
XX

AAO03855;

06-NOV-2001 (first entry)

Human polypeptide SEQ ID NO 17747.

Human: cytokine; cell proliferation; cell differentiation; gene therapy;

tissue growth factor; stem cell growth factor; haematopoiesis;

nervous system disorders; arthritis; inflammation.

Homo sapiens.

MO200164835-A2.

07-SEP-2001.

26-FEB-2001; 2001MO-US004927.

28-FEB-2000; 2000US-00515126.

18-MAY-2000; 2000US-00577409.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-514838/56.

N-PSDB; AAI83786.

Claim 20; SEQ ID NO 17747; 1399pp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pcc_sequences
XX
SQ Sequence 108 AA;

Query Match 89.3%; Score 25; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
||||:
Db 54 HYAMA 58

RESULT 32
ADB07666
ID ADB07666 standard; protein; 113 AA.

AC ADB07666;

XX 20-NOV-2003 (first entry)

XX Allotococcus oclis antigenic protein SEQ ID NO:1606.

XX Allotococcus oclidis; antigenic protein; immunogenic; immunisation;
XX gene therapy; Gram-positive bacterium; infection.

XX Allotococcus oclis.

XX WO2003048304-A2.

XX 12-JUN-2003.

XX 25-NOV-2002; 2002WO-US036123.

XX 29-NOV-2001; 2001US-033777P.

XX 18-NOV-2002; 2002US-0426742P.

XX (AMMP) WYETH HOLDINGS CORP.

XX Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;

XX WPI: 2003-505284/47.

XX N-PSDB; ADB07665.

XX New Allotococcus oclidis polynucleotides and polypeptides, useful for
XX treating and diagnosing diseases, drug screening assays and monitoring of
XX effects during drug clinical trials.

XX Claim 33; SEQ ID NO 1606; 1019pp; English.

XX The present invention describes an isolated polynucleotide (I) of
XX Allotococcus oclidis genomic DNA, which encodes an antigenic protein.
XX Allotococcus oclidis is a Gram-positive bacterium. Also described: (1)
XX an isolated polypeptide that is encoded by the polynucleotide (I); (2) an
XX expression vector comprising the novel isolated polynucleotide (I), its
XX complement, degenerate variant or fragment; (3) a genetically engineered
XX host cell, transfected, transformed or infected with the vector of (2);
XX (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
XX composition comprising the polypeptide, its complement, biological
XX equivalent or fragment, or the polynucleotide that is comprised in the
XX expression vector; (6) a pharmaceutical composition comprising the
XX polypeptide of (1) and a carrier; (7) a protein chip comprising an array
XX of the polypeptides of (1), their biological equivalent or fragment; (8)
XX immunising against Allotococcus oclidis by administering to a host the
XX immunogenic composition; (9) detecting and/or identifying Allotococcus
XX oclidis in the biological sample; (10) a kit comprising a container
XX containing the novel polynucleotide, its degenerate variant or fragment,
XX or the antibody of (4); and (11) producing a polypeptide by culturing the
XX genetically engineered host cell under conditions suitable to produce the
XX polypeptide from the culture. (I) can be used in gene therapy. The

CC polynucleotides, polypeptides, antibodies and compositions of the present
CC invention can be used for treating and diagnosing diseases, drug
CC screening assays and monitoring of effects during drug clinical trials.
CC The polynucleotides are useful for expressing and detecting Allotococcus
CC oclidis. The present sequence represents an Allotococcus oclidis
CC antigen protein from the present invention.
XX

SQ Sequence 113 AA;

Query Match 89.3%; Score 25; DB 6; Length 113;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
||||:
Db 74 HYALS 78

RESULT 33
AAG81907
ID AAG81907 standard; protein; 116 AA.

XX AAG81907;

XX 03-SEP-2001 (first entry)

XX S. epidermidis open reading frame protein sequence SEQ ID NO:908.

XX Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination;
XX endocarditis.

XX Staphylococcus epidermidis.

XX WO200134809-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US030782.

XX 09-NOV-1999; 99US-0164258P.

XX (GLAX) GLAXO GROUP LTD.

XX Kimmeryly WJ;

XX WPI: 2001-316495/33.

XX N-PSDB; AAG81907.

XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis.

XX Claim 18; Page 271; 2189pp; English.

XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in AAH81454 to AAG81120, from Staphylococcus epidermidis. (1)
XX and (II) can have antibacterial activity and therefore can be used in
XX vaccination. The nucleic acids (I) may be used to produce the S.
XX epidermidis polypeptides (II) via the production of vectors containing
XX them which are used to produce hosts cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX AAH53090 represent specifically claimed S. epidermidis genomic DNA
XX polynucleotide sequences from the present invention. AAH55091 to AAH55098
XX represent oligonucleotide sequences and primers which are used in the
XX exemplification of the present invention. N.B. The present invention
XX specifically claims all the polynucleotide sequences given in the
XX sequence listing of the present specification, however the sequence
XX listing only goes up to SEQ ID NO:4454 so even though sequences are given
XX in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
XX for SEQ ID NO:4455 to 4464

XX Sequence 116 AA;
SQ
Query Match 89.3%; Score 25; DB 4; Length 116;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 HYAMS 5
DB 34 HYAMT 38
RESULT 34
ABU49557
ID ABU49557 standard; protein; 126 AA.
XX
XX ABU49557;
AC
XX 19-JUN-2003 (first entry)
XX
XX Protein encoded by Prokaryotic essential gene #35084.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Vibrio cholerae.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zyskind JW;
XX Wall D, Treweek JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX N-PSDB; ACAS3427.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids, required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 77481; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 126 AA;
Query Match 89.3%; Score 25; DB 6; Length 126;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 HYAMS 5
DB 115 HYAMA 119
RESULT 35
ADB07674
ID ADB07674 standard; protein; 133 AA.
XX
XX ADB07674;
AC
XX 20-NOV-2003 (first entry)
XX
XX Allotiococcus oclitis antigenic protein SEQ ID NO:1614.
XX
XX Allotiococcus oclitis; antigenic protein; immunogenic; immunisation;
XX KM gene therapy; Gram-positive bacterium; infection.
XX
XX Allotiococcus oclitis.
XX
XX WO2003048304-A2.
XX
XX 12-JUN-2003.
XX
XX 25-NOV-2002; 2002WO-US036123.
XX
XX 29-NOV-2001; 2001US-0333777P.
XX 18-NOV-2002; 2002US-0426742P.
XX
XX (AMHP) WYETH HOLDINGS CORP.
XX
XX Fletcher LD, McMichael JC, Russell DP, Zagureky RJ;
XX WPI; 2003-505284/47.
XX N-PSDB; ADB07673.
XX
XX New Allotiococcus oclitis polynucleotides and polypeptides, useful for
XX treating and diagnosing diseases, drug screening assays and monitoring of
XX effects during drug clinical trials.
XX
XX Claim 33; SEQ ID NO 1614; 1019pp; English.
XX
XX The present invention describes an isolated polynucleotide (1) of
XX Allotiococcus oclitis genomic DNA, which encodes an antigenic protein.
XX Allotiococcus oclitis is a Gram-positive bacterium. Also described: (1)
XX an isolated polypeptide that is encoded by the polynucleotide (1); (2) an
XX expression vector comprising the novel isolated polynucleotide (1), its
XX complement, degenerate variant or fragment; (3) a genetically engineered
XX host cell, transfected, transformed or infected with the vector of (2);
XX (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
XX composition comprising the polypeptide, its complement, biological
XX equivalent or fragment, or the polynucleotide that is comprised in the
XX expression vector; (6) a pharmaceutical composition comprising the
XX polypeptide of (1) and a carrier; (7) a protein chip comprising an array
XX of the polypeptides of (1), their biological equivalent or fragment; (8)
XX immunising against Allotiococcus oclitis by administering to a host the

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SO Sequence 146 AA;

Query Match 89.3%; Score 25; DB 4; Length 146;
Best Local Similarity 80.0%; Pred. No. 5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
Db 74 HVALS 78

RESULT 38

ID AAU17373 standard; protein; 150 AA.

XX AAU17373;

DT 07-NOV-2001 (first entry)

XX Novel signal transduction pathway protein, Seq ID 938.

XX Neuroprotective; cytoskeletal; dermatological; immunosuppressive; tumour;
XX antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
XX immune system disorder; rheumatoid arthritis; inflammatory condition;
XX organ transplant rejection; infection; hepatitis C; blood disorder;
XX sickle cell anemia; hyperproliferative disorder; Gaucher's disease;
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
XX cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
XX reproductive system; gastrointestinal; liver disorder; AIDS;
XX acquired immune deficiency syndrome.

XX Homo sapiens.

OS WO200154733-A1.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001312.

XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217486P.
PR 14-JUL-2000; 2000US-0218280P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0244612P.
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PR 08-NOV-2000; 2000US-0246526P.
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PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.
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PR 08-NOV-2000; 2000US-0246613P.
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PR 17-NOV-2000; 2000US-0249215P.
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PR 08-DEC-2000; 2000US-0251889P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI, 2001-465460/50.
XX N-PSDB; AAS27290.
DR
DR
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX
XX
PS Claim 1; SEQ ID NO 938; 880pp; English.
PS
XX
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, hemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (e.g.
CC Down syndrome), ischemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
CC AAU17683 represent novel signal transduction pathway protein, amino acid
CC sequences of the invention
XX

Query Match 89.3%; Score 25; DB 4; Length 150;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 65 HYALS 69
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AC
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XX 04-DEC-2003 (first entry)
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XX Human novel protein #315.
DE
XX
XX human; autoimmune disease; Parkinson's disease; silicosis;
XX gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
XX immunosuppressive agent; adjuvant; enhance immune response;
XX higher affinity antibody induction;
XX increased serum immunoglobulin concentration.
XX
XX Homo sapiens.
XX
XX US2002168711-A1.
PD
XX 14-NOV-2002.
XX
XX 17-JAN-2001; 2001US-00764868.
PF
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XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 02-OCT-2000; 2000US-0237040P.
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 XX
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI; 2003-719985/68.
 DR N-PSDB; ADB93458.
 XX
 PT New isolated polypeptide useful for diagnosing and treating
 PT immunosuppressive conditions such as autoimmune disease and Parkinson's
 PT disease.
 XX
 PS Claim 11, SEQ ID NO 938; 345pp; English.
 XX
 CC The invention relates to an isolated polypeptide. The polypeptide is
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition in a subject, by determining the presence or
 CC amount of expression of the polypeptide in a biological sample and
 CC diagnosing a pathological condition or a susceptibility to a pathological
 CC condition based on the presence or amount of expression of the
 CC polypeptide. The polypeptide is also useful for identifying a binding
 CC partner to the polypeptide, which involves contacting the polypeptide
 CC with a binding partner and determining whether the binding partner
 CC effects an activity of the polypeptide. The polypeptide or the nucleic
 CC acid encoding the polypeptide is useful for preventing, treating, or
 CC ameliorating a medical condition, which involves administering the
 CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
 CC is useful for diagnosing a pathological condition or a susceptibility to
 CC a pathological condition in a subject, which involves determining the
 CC presence or absence of a mutation in the nucleic acid, and diagnosing a
 CC pathological condition or susceptibility to a pathological condition
 CC based on the presence or absence of the mutation. The polypeptide, the
 CC nucleic acid and an antibody to the polypeptide are useful for treating
 CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
 CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,
 CC the nucleic acid and the antibody are useful as immunosuppressive agents,
 CC as adjuvants to enhance immune responses, and as agents to induce higher
 CC affinity antibodies and increase serum immunoglobulin concentrations. The
 CC present sequence represents the amino acid sequence of a novel human
 CC protein. Note: The sequence data for this patent did not form part of the
 CC printed specification but was obtained in electronic format direct from
 CC USPTO at seqdata.uspto.gov/sequence.html?docID=20020168711.
 CC
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 SQ Sequence 150 AA;
 Query Match 89.3%; Score 25; DB 7; Length 150;
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 Db 65 HYALS 69
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 ID ABG21786 standard; protein; 164 AA.
 AC ABG21786;
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 DT 18-FEB-2002 (first entry)

XX
 DE Novel human diagnostic protein #21777.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSSEQ INC.
 PA
 PI Drmanac RT, Liu C, Tang YF;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS85973.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 52145; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
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 SQ Sequence 164 AA;
 Query Match 89.3%; Score 25; DB 4; Length 164;
 Best Local Similarity 80.0%; Pred. No. 5.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 Db 18 HYALS 22
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 Job time : 17.1966 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 17, 2004, 18:13:27 ; Search time 3.03371 Seconds
(without alignments)
109.302 Million cell updates/sec

Title: US-10-089-500-3
Perfect score: 28
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Listing first 45 summaries

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SUMMARIES

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2	28	100.0	130	4	US-09-225-322B-8 Sequence 8, Appl1
3	28	100.0	130	4	US-09-225-322B-18 Sequence 18, Appl1
4	28	100.0	130	4	US-09-764-304-8 Sequence 8, Appl1
5	28	100.0	130	4	US-09-764-304-18 Sequence 18, Appl1
6	28	100.0	211	4	US-09-270-767-34278 Sequence 34278, A
7	28	100.0	211	4	US-09-270-767-49495 Sequence 49495, A
8	28	100.0	351	4	US-09-270-767-42774 Sequence 42774, A
9	28	100.0	424	4	US-09-824-734-4 Sequence 4, Appl1
10	28	100.0	514	4	US-09-252-991A-20338 Sequence 20338, A
11	25	89.3	23	3	US-08-335-865J-4 Sequence 4, Appl1
12	25	89.3	116	4	US-09-710-279-908 Sequence 908, App
13	25	89.3	306	4	US-09-248-796A-18665 Sequence 18665, A
14	25	89.3	308	4	US-09-710-279-1072 Sequence 1072, Ap
15	25	89.3	308	4	US-09-710-279-2706 Sequence 2706, Ap
16	25	89.3	318	3	US-09-134-001C-3852 Sequence 3852, Ap
17	25	89.3	318	4	US-09-248-796A-14325 Sequence 14325, A
18	25	89.3	348	4	US-09-270-767-44839 Sequence 44839, A
19	25	89.3	352	4	US-09-711-164-448 Sequence 448, App
20	25	89.3	359	4	US-09-543-681A-5431 Sequence 5431, Ap
21	25	89.3	371	3	US-09-500-569-16 Sequence 16, Appl
22	25	89.3	371	4	US-09-971-823B-16 Sequence 16, Appl
23	25	89.3	410	4	US-09-489-039A-10078 Sequence 10078, A
24	25	89.3	439	4	US-08-311-731A-48 Sequence 48, Appl
25	25	89.3	440	4	US-09-543-681A-8179 Sequence 8179, Ap
26	25	89.3	440	4	US-09-248-796A-19817 Sequence 19817, A
27	25	89.3	473	4	US-09-328-352-4712 Sequence 4712, Ap

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29	25	89.3	494	4	US-09-670-141-2 Sequence 2, Appl1
30	25	89.3	566	3	US-08-335-865J-9 Sequence 9, Appl1
31	25	89.3	593	3	US-08-335-865J-21 Sequence 21, Appl
32	25	89.3	606	3	US-08-335-865J-20 Sequence 20, Appl
33	25	89.3	628	4	US-09-252-991A-24741 Sequence 24741, A
34	25	89.3	735	3	US-09-147-236-7 Sequence 7, Appl1
35	25	89.3	735	4	US-09-522-474-7 Sequence 7, Appl1
36	24	85.7	46	4	US-09-621-976-6089 Sequence 6089, Ap
37	24	85.7	61	4	US-09-489-039A-13625 Sequence 13625, A
38	24	85.7	63	4	US-09-270-767-62479 Sequence 62479, A
39	24	85.7	68	4	US-09-248-796A-26555 Sequence 26555, A
40	24	85.7	77	4	US-09-248-796A-504 Sequence 504, App
41	24	85.7	88	3	US-08-958-136-4 Sequence 4, Appl1
42	24	85.7	140	3	US-08-943-136-4 Sequence 4, Appl1
43	24	85.7	140	3	US-08-973-518-4 Sequence 43, Appl
44	24	85.7	144	4	US-09-394-455-43 Sequence 45, Appl
45	24	85.7	144	4	US-09-394-455-45 Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-770-834-6
; Sequence 6, Application US/09770834
; Patent No. 6684162
; GENERAL INFORMATION:
; APPLICANT: Parfitts, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBSTITIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/09/770,834
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-770-834-6

Query Match 100.0% Score 28; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 106 HYAMS 110

RESULT 2
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; Sequence 8, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASBEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05

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; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
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; SEQ ID NO 8
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-8

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Query Match          100.0%; Score 28; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      41 HYAMS 45

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; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
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; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
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; PRIOR FILING DATE: 1992-09-17
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US-09-225-322B-18

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
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; EARLIER FILING DATE: 1995-05-31
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; EARLIER FILING DATE: 1994-08-17
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; OTHER INFORMATION: cDNA KM-641
US-09-764-304-8

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; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 09/225,322
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; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18

```

/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: cDNA KM-641
US-09-764-304-18

Query Match 100.0%; Score 28; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 41 HYAMS 45

RESULT 6
US-09-270-767-34278
/ Sequence 34278, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 34278
/ LENGTH: 211
/ TYPE: PRT
/ ORGANISM: *Drosophila melanogaster*
/ FEATURE:
/ OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34278

Query Match 100.0%; Score 28; DB 4; Length 211;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 154 HYAMS 158

RESULT 7
US-09-270-767-49495
/ Sequence 49495, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 49495
/ LENGTH: 211
/ TYPE: PRT
/ ORGANISM: *Drosophila melanogaster*
/ FEATURE:
/ OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49495

Query Match 100.0%; Score 28; DB 4; Length 211;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 154 HYAMS 158

RESULT 8
US-09-270-767-42774
/ Sequence 42774, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 42774
/ LENGTH: 351
/ TYPE: PRT
/ ORGANISM: *Drosophila melanogaster*
/ FEATURE:
/ OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42774

Query Match 100.0%; Score 28; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 247 HYAMS 251

RESULT 9
US-09-824-734-4
/ Sequence 4, Application US/09824734
/ Patent No. 6727408
/ GENERAL INFORMATION:
/ APPLICANT: ZHU, JIAN-KANG
/ APPLICANT: SHI, HUAZHONG
/ APPLICANT: ISHITANI, MANABU
/ APPLICANT: STEVENSON, BECKY
/ TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS
/ FILE REFERENCE: 205644US20
/ CURRENT APPLICATION NUMBER: US/09/824,734
/ CURRENT FILING DATE: 2001-04-04
/ PRIOR APPLICATION NUMBER: US 60/194,648
/ PRIOR FILING DATE: 2000-04-04
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 4
/ LENGTH: 424
/ TYPE: PRT
/ ORGANISM: *Pseudomonas aeruginosa*
US-09-824-734-4

Query Match 100.0%; Score 28; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 272 HYAMS 276

RESULT 10
US-09-252-991A-20338
/ Sequence 20338, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20338
LENGTH: 514
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20338

Query Match 100.0%; Score 28; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 362 HYAMS 366

RESULT 11
US-08-335-865J-4
Sequence 4; Application US/08335865J
Patent No. 6107472
GENERAL INFORMATION:
APPLICANT: Stacke, Steven A.; Hovens, Christopher M.,
APPLICANT: Wilks, Andrew F.
TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Ave
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: ASCII/Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,865J
FILING DATE: 19-January-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00210
FILING DATE: 10-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PL2358
FILING DATE: 11-May-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6107472man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD-5277
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 23
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-335-865J-4

Query Match 89.3%; Score 25; DB 3; Length 23;
Best Local Similarity 80.0%; Pred. No. 16;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 18 HYALS 22

RESULT 12
US-09-710-279-908
Sequence 908; Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 908
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-908

Query Match 89.3%; Score 25; DB 4; Length 116;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 34 HYAMT 38

RESULT 13
US-09-248-796A-16865
Sequence 16865; Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16865
LENGTH: 306
TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: UNSURE
LOCATION: (6), (51)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-16865

Query Match 89.3%; Score 25; DB 4; Length 306;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 83 HYALS 87

RESULT 14
US-09-710-279-1072
Sequence 1072; Application US/09710279
Patent No. 6703492

GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1072
LENGTH: 308
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-1072

Query Match 89.3%; Score 25; DB 4; Length 308;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HYAMS 5
Db 209 HYALS 213

RESULT 15
US-09-710-279-2706
Sequence 2706, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2706
LENGTH: 308
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-2706

Query Match 89.3%; Score 25; DB 4; Length 308;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HYAMS 5
Db 209 HYALS 213

RESULT 16
US-09-134-001C-3852
Sequence 3852, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3852
LENGTH: 318
TYPE: PR1
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3852

Query Match 89.3%; Score 25; DB 3; Length 318;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HYAMS 5
Db 219 HYALS 223

RESULT 17
US-09-248-796A-14325
Sequence 14325, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196,132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14325
LENGTH: 318
TYPE: PR1
ORGANISM: Candida albicans
US-09-248-796A-14325

Query Match 89.3%; Score 25; DB 4; Length 318;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HYAMS 5
Db 199 HYALS 203

RESULT 18
US-09-270-767-44839
Sequence 44839, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44839
LENGTH: 348
TYPE: PR1
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44839

Query Match 89.3%; Score 25; DB 4; Length 348;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||:
Db 193 HYAMA 197

RESULT 19
US-09-711-164-448
; Sequence 448, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlson, Karl
; APPLICANT: Zykkind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERAPY
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711,164
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 352
; TYPE: PRF
; ORGANISM: Escherichia coli
US-09-711-164-448

Query Match 89.3%; Score 25; DB 4; Length 352;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||:
Db 245 HYAMT 249

RESULT 20
US-09-543-681A-5431
; Sequence 5431, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5431
; LENGTH: 359
; TYPE: PRF
; ORGANISM: Proteus mirabilis
US-09-543-681A-5431

Query Match 89.3%; Score 25; DB 4; Length 359;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||:
Db 250 HYAMT 254

RESULT 21
US-09-500-569-16
; Sequence 16, Application US/09500569
; Patent No. 6329204
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafaleki, Antoni
; APPLICANT: Shen, Jennie

; TITLE OF INVENTION: Plant Caffeic acid 3-O-methyltransferase Homologs
; FILE REFERENCE: BBI327 US NA
; CURRENT APPLICATION NUMBER: US/09/500,569
; CURRENT FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: 60/119,587
; EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 371
; TYPE: PRF
; ORGANISM: Oryza sativa
US-09-500-569-16

Query Match 89.3%; Score 25; DB 3; Length 371;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||:
Db 291 HYALS 295

RESULT 22
US-09-971-823B-16
; Sequence 16, Application US/09971823B
; Patent No. 6610521
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
; FILE REFERENCE: BBI327 US NA
; CURRENT APPLICATION NUMBER: US/09/971,823B
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/119,587
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 371
; TYPE: PRF
; ORGANISM: Oryza sativa
US-09-971-823B-16

Query Match 89.3%; Score 25; DB 4; Length 371;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||:
Db 291 HYALS 295

RESULT 23
US-09-489-039A-10078
; Sequence 10078, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10078
; LENGTH: 410
; TYPE: PRF
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10078

Query Match 89.3%; Score 25; DB 4; Length 410;

Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 391 HYAMA 395

RESULT 24
US-08-311-731A-48
Sequence 48, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 439 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LAPRAE
US-08-311-731A-48
Query Match 89.3%; Score 25; DB 4; Length 439;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 366 HYAMT 370
RESULT 25
US-09-543-681A-8179
Sequence 8179, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 8179
LENGTH: 440
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-8179

Query Match 89.3%; Score 25; DB 4; Length 440;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 106 HYAMN 110

RESULT 26
US-09-248-796A-19817
Sequence 19817, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19817
LENGTH: 440
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-19817

Query Match 89.3%; Score 25; DB 4; Length 440;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 344 HYAMN 348

RESULT 27
US-09-328-352-4712
Sequence 4712, Application US/09328352
Patent No. 6562938
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4712
LENGTH: 473
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4712

Query Match 89.3%; Score 25; DB 4; Length 473;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 111

Db 462 HYALS 466

RESULT 28

US-09-198-956-2
; Sequence 2, Application US/09198956
; Patent No. 6165769
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schullein, Martin
; APPLICANT: Lange, Niels Erik K.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Schmitt, Kirk
; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
; FILE REFERENCE: 5377.200-US
; CURRENT APPLICATION NUMBER: US/09/198,956
; EARLIER FILING DATE: 1998-11-24
; EARLIER APPLICATION NUMBER: 1344/97
; EARLIER FILING DATE: 1997-11-24
; EARLIER APPLICATION NUMBER: 60/067,240
; EARLIER FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-198-956-2

Query Match 89.3%; Score 25; DB 3; Length 494;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
|||:
Db 99 HYALS 103

RESULT 29

US-09-670-141-2
; Sequence 2, Application US/09670141
; Patent No. 6429000
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schullein, Martin
; APPLICANT: Lange, Niels Erik K.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Schmitt, Kirk
; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
; FILE REFERENCE: 5377.200-US
; CURRENT APPLICATION NUMBER: US/09/670,141
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/198,956
; PRIOR FILING DATE: 1998-11-24
; PRIOR APPLICATION NUMBER: 1344/97
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/067,240
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-670-141-2

Query Match 89.3%; Score 25; DB 4; Length 494;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5

Db 99 HYALS 103

RESULT 30

US-08-335-865J-9
; Sequence 9, Application US/08335865J
; Patent No. 6107472
; GENERAL INFORMATION:
; APPLICANT: Stackey, Steven A.; Hovens, Christopher M.,
; APPLICANT: Wilks, Andrew F.
; TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Ave
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: ASCII/Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,865J
; FILING DATE: 19-January-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU93/00210
; FILING DATE: 10-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PL2358
; FILING DATE: 11-May-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6107472man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD-5277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3100
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 566
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE: mouse
US-08-335-865J-9

Query Match 89.3%; Score 25; DB 3; Length 566;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
|||:
Db 49 HYALS 53

RESULT 31

US-08-335-865J-21
; Sequence 21, Application US/08335865J
; Patent No. 6107472
; GENERAL INFORMATION:
; APPLICANT: Stackey, Steven A.; Hovens, Christopher M.,
; APPLICANT: Wilks, Andrew F.
; TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Ave
; CITY: New York
; STATE: New York

COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: ASCII/wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,865J
FILING DATE: 19-January-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00210
FILING DATE: 10-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PL2358
FILING DATE: 11-May-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6107472man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD-5277
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 593
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: human
US-08-335-865J-21

Query Match 89.3%; Score 25; DB 3; Length 593;
Best Local Similarity 80.0%; Pred. No. 5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 76 HYALS 80

RESULT 32
US-08-335-865J-20
Sequence 20, Application US/08335865J
Patent No. 6107472
GENERAL INFORMATION:
APPLICANT: Stackel, Steven A.; Hovens, Christopher M.,
APPLICANT: Wilks, Andrew F.
TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Ave
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: ASCII/wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,865J
FILING DATE: 19-January-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00210
FILING DATE: 10-May-1993
PRIOR APPLICATION DATA: PL2358
FILING DATE: 11-May-1992

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6107472man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD-5277
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 606
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: human
US-08-335-865J-20

Query Match 89.3%; Score 25; DB 3; Length 606;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 90 HYALS 94

RESULT 33
US-09-252-991A-24741
Sequence 24741, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24741
LENGTH: 628
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24741

Query Match 89.3%; Score 25; DB 4; Length 628;
Best Local Similarity 80.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 604 HYAMA 608

RESULT 34
US-09-147-236-7
Sequence 7, Application US/09147236A
Patent No. 6316251
GENERAL INFORMATION:
APPLICANT: TONOUCHI, Naoto
APPLICANT: TSUCHIDA, Takayasu
APPLICANT: YOSHINAGA, Fumihito
APPLICANT: TAHARA, Naoki
APPLICANT: HAYASHI, Takahisa
TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
FILE REFERENCE: 6537-011-0PCT
CURRENT APPLICATION NUMBER: US/09/147,236A
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/JP97/03633
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 12

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Acetobacter xylinum
; FEATURE:
; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, t, or
; US-09-147-236-7

Query Match
Best Local Similarity 89.3%; Score 25; DB 3; Length 735;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 5
Db 199 HYAMN 203

RESULT 35
US-09-522-474-7
; Sequence 7, Application US/09522474
; Patent No. 6573076
; GENERAL INFORMATION:
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: TSUCHIDA, Takayasu
; APPLICANT: YOSHINAGA, Fumihiko
; APPLICANT: TAHARA, Naoki
; APPLICANT: HAYASHI, Takahisa
; TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
; FILE REFERENCE: 6537-011-0PCT
; CURRENT APPLICATION NUMBER: US/09/522,474
; CURRENT FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US/09/147,236
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/JP97/03633
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Acetobacter xylinum
; FEATURE:
; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, t, or
; OTHER INFORMATION: c
; US-09-522-474-7

Query Match
Best Local Similarity 89.3%; Score 25; DB 4; Length 735;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 5
Db 199 HYAMN 203

RESULT 36
US-09-095-881-14
; Sequence 14, Application US/09095881
; Patent No. 6489137
; GENERAL INFORMATION:
; APPLICANT: Sealey, Todd
; TITLE OF INVENTION: DETECTION OF LOSS OF THE WILD-TYPE
; TITLE OF INVENTION: HUBB1 GENE
; FILE REFERENCE: 1405.003 / 200130.437
; CURRENT APPLICATION NUMBER: US/09/095,881
; CURRENT FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 46
; TYPE: PRT
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; ORGANISM: Homo sapien
; US-09-095-881-14

Query Match
Best Local Similarity 85.7%; Score 24; DB 4; Length 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4
Db 28 HYAM 31

RESULT 37
US-09-621-976-6089
; Sequence 6089, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Joubert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6089
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 29
; OTHER INFORMATION: Xaa = *, Glu
; US-09-621-976-6089

Query Match
Best Local Similarity 85.7%; Score 24; DB 4; Length 61;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4
Db 46 HYAM 49

RESULT 38
US-09-489-039A-13625
; Sequence 13625, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13625
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-13625

Query Match
Best Local Similarity 85.7%; Score 24; DB 4; Length 63;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4
Db 23 HYAM 26
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RESULT 39
US-09-270-767-62479
; Sequence 62479, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 62479
; LENGTH: 68
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-62479

Query Match 85.7%; Score 24; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4
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Db 54 HYAM 57

RESULT 40
US-09-248-796A-26555
; Sequence 26555, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26555
; LENGTH: 77
; TYPE: PRT
; ORGANISM: *Candida albicans*
US-09-248-796A-26555

Query Match 85.7%; Score 24; DB 4; Length 77;
Best Local Similarity 80.0%; Pred. No. 98;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||
Db 72 HYAMS 76

Search completed: December 17, 2004, 18:32:07
Job time : 4.03371 secs

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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: December 17, 2004, 18:20:33 / Search time 9.66292 Seconds
(without alignments)
185.159 Million cell updates/sec

Title: US-10-089-500-3

Perfect score: 28

Sequence: 1 HYAMS 5

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	28	100.0	119	10	US-09-770-834-6
3	28	100.0	119	15	US-10-282-122A-44196
4	28	100.0	119	15	US-10-282-122A-71569
5	28	100.0	119	15	US-10-717-138-6
6	28	100.0	130	9	US-09-764-304-8
7	28	100.0	130	9	US-09-764-304-18
8	28	100.0	130	14	US-10-265-713-8
9	28	100.0	130	14	US-10-265-713-18
10	28	100.0	130	14	US-10-166-626-8
11	28	100.0	130	14	US-10-166-626-18
12	28	100.0	412	14	US-10-369-493-10250
13	28	100.0	424	9	US-09-824-734-4

14	28	100.0	424	16	US-10-749-386-4	Sequence 4, Appl1
15	28	100.0	1031	16	US-10-437-963-189155	Sequence 189155,
16	25	89.3	53	15	US-10-424-599-24063	Sequence 24063,
17	25	89.3	54	17	US-10-425-115-279811	Sequence 279811,
18	25	89.3	57	15	US-10-424-599-181420	Sequence 181420,
19	25	89.3	57	17	US-10-425-115-249920	Sequence 249920,
20	25	89.3	58	15	US-10-424-599-177790	Sequence 177790,
21	25	89.3	58	15	US-10-335-977-8261	Sequence 8261, Ap
22	25	89.3	70	15	US-10-424-599-214263	Sequence 214263,
23	25	89.3	77	15	US-10-424-599-199143	Sequence 199143,
24	25	89.3	84	17	US-10-425-115-313005	Sequence 313005,
25	25	89.3	85	15	US-10-424-599-275379	Sequence 275379,
26	25	89.3	86	15	US-10-424-599-180930	Sequence 180930,
27	25	89.3	86	15	US-10-424-599-231987	Sequence 231987,
28	25	89.3	89	15	US-10-424-599-184650	Sequence 184650,
29	25	89.3	99	17	US-10-425-115-270245	Sequence 270245,
30	25	89.3	100	16	US-10-437-963-172988	Sequence 172988,
31	25	89.3	107	16	US-10-437-963-155791	Sequence 155791,
32	25	89.3	126	15	US-10-282-122A-77481	Sequence 77481, A
33	25	89.3	131	16	US-10-437-963-106924	Sequence 106924,
34	25	89.3	131	17	US-10-425-115-360208	Sequence 360208,
35	25	89.3	135	15	US-10-424-599-207366	Sequence 207366,
36	25	89.3	136	15	US-10-424-599-177566	Sequence 177566,
37	25	89.3	148	15	US-10-424-599-188149	Sequence 188149,
38	25	89.3	150	9	US-09-764-868-938	Sequence 938, App
39	25	89.3	174	17	US-10-425-115-225898	Sequence 225898,
40	25	89.3	180	15	US-10-275-589-3	Sequence 3, Appl1
41	25	89.3	181	15	US-10-275-589-2	Sequence 2, Appl1
42	25	89.3	191	15	US-10-275-589-1	Sequence 1, Appl1
43	25	89.3	191	17	US-10-425-115-269047	Sequence 269047,
44	25	89.3	192	16	US-10-437-963-203843	Sequence 203843,
45	25	89.3	201	16	US-10-437-963-117523	Sequence 117523,

ALIGNMENTS

RESULT 1
US-09-771-383-5
; Sequence 5, Application US/09771383
; Patent No. US20020094562A1
; GENERAL INFORMATION:
; APPLICANT: Parfitt, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACTL CARRIER PROTEIN SYNTHASE
; FILE REFERENCE: 2368/12
; CURRENT APPLICATION NUMBER: US/09771,383
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/178,639
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Staphylococcus
US-09-771-383-5

Query Match 100.0%; Score 28; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 106 HYAMS 110

RESULT 2
US-09-770-834-6

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/ Sequence 6, Application US/09770834
/ Publication No. US20030211588A1
/ GENERAL INFORMATION:
/ APPLICANT: Parrie, Kevin
/ APPLICANT: Somers, William
/ APPLICANT: Tam, Amy
/ APPLICANT: Lin, Laura
/ APPLICANT: Stahl, Mark
/ APPLICANT: Powers, Robert
/ APPLICANT: Xu, Guan-Yi
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
/ TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
/ FILE REFERENCE: 2368/14
/ CURRENT APPLICATION NUMBER: US/09/770,834
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US 60/202,466
/ PRIOR FILING DATE: 2000-05-08
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 6
/ LENGTH: 119
/ TYPE: PRT
/ ORGANISM: Staphylococcus sp.
US-09-770-834-6
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Query Match          100.0%; Score 28; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HYAMS 5

DB 106 HYAMS 110

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RESULT 3
US-10-282-122A-44196
/ Sequence 44196, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zysek, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ PRIOR FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
```

```
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 44196
/ LENGTH: 119
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-282-122A-44196
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Query Match          100.0%; Score 28; DB 15; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HYAMS 5

DB 106 HYAMS 110

```
RESULT 4
US-10-282-122A-71569
/ Sequence 71569, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zysek, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ PRIOR FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 71569
/ LENGTH: 119
/ TYPE: PRT
/ ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-71569
```

```
Query Match          100.0%; Score 28; DB 15; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


Qy 1 HYAMS 5
|||||
Db 107 HYAMS 111

RESULT 5

US-10-717-138-6
; Sequence 6, Application US/10717138
; Publication No. US20040078147A1
; GENERAL INFORMATION:
; APPLICANT: Parits, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/10/717,138
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/770,834
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-10-717-138-6

Query Match 100.0%; Score 28; DB 15; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
|||||
Db 106 HYAMS 110

RESULT 6

US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8

; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA KM-641
US-09-764-304-8

Query Match 100.0%; Score 28; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
|||||
Db 41 HYAMS 45

RESULT 7

US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA KM-641
US-09-764-304-18

Query Match 100.0%; Score 28; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
|||||
Db 41 HYAMS 45

RESULT 8

US-10-265-713-8
; Sequence 8, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101

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; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-8

```

```

Query Match      100.0%; Score 28; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 HYAMS 5
Db      41 HYAMS 45

```

```

RESULT 9
US-10-265-713-18
; Sequence 18, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-18

```

```

Query Match      100.0%; Score 28; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 HYAMS 5
Db      41 HYAMS 45

```

```

RESULT 10
US-10-166-626-8
; Sequence 8, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-8

```

```

Query Match      100.0%; Score 28; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 HYAMS 5
Db      41 HYAMS 45

```

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RESULT 11
US-10-166-626-18
; Sequence 18, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674

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;; PRIOR FILING DATE: 1992-09-17
;; PRIOR APPLICATION NUMBER: JP 3-238375
;; PRIOR FILING DATE: 1991-09-18
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 18
;; LENGTH: 130
;; TYPE: PRF
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-18

Query Match 100.0%; Score 28; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 41 HYAMS 45

RESULT 12
US-10-369-493-10250
; Sequence 10250, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10250
; LENGTH: 412
; TYPE: PRF
; ORGANISM: Cytophaga hutchinsonii
US-10-369-493-10250

Query Match 100.0%; Score 28; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 390 HYAMS 394

RESULT 13
US-09-824-734-4
; Sequence 4, Application US/09824734
; Patent No. US20020083485A1
; GENERAL INFORMATION:
; APPLICANT: ZHU, JIAN-KANG
; APPLICANT: SHI, HUAZHONG
; APPLICANT: ISHITANI, MANABU
; APPLICANT: STEVENSON, BECKY
; TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS
; FILE REFERENCE: 205644US20
; CURRENT APPLICATION NUMBER: US/09/824,734
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/194,648
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

;; LENGTH: 424
;; TYPE: PRF
;; ORGANISM: Pseudomonas aeruginosa
US-09-824-734-4

Query Match 100.0%; Score 28; DB 9; Length 424;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 272 HYAMS 276

RESULT 14
US-10-749-386-4
; Sequence 4, Application US/10749386
; Publication No. US20040186276A1
; GENERAL INFORMATION:
; APPLICANT: ZHU, JIAN-KANG
; APPLICANT: SHI, HUAZHONG
; APPLICANT: ISHITANI, MANABU
; APPLICANT: STEVENSON, BECKY
; TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS
; FILE REFERENCE: 205644US20
; CURRENT APPLICATION NUMBER: US/10/749,386
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US/09/824,734
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/194,648
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 424
; TYPE: PRF
; ORGANISM: Pseudomonas aeruginosa
US-10-749-386-4

Query Match 100.0%; Score 28; DB 16; Length 424;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 272 HYAMS 276

RESULT 15
US-10-437-963-189155
; Sequence 189155, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189155
; LENGTH: 1031
; TYPE: PRF
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85691C.1.pep

US-10-437-963-189155

Query Match 100.0%; Score 28; DB 16; Length 1031;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 485 HYAMS 489

RESULT 16

US-10-424-599-240643
; Sequence 240643, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240643
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(53)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59328C.1.pep
US-10-424-599-240643

Query Match 89.3%; Score 25; DB 15; Length 53;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 40 HYAMA 44

RESULT 17

US-10-425-115-279811
; Sequence 279811, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 279811
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_186768C.1.pep
US-10-425-115-279811

Query Match 89.3%; Score 25; DB 17; Length 54;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 48 HYAMS 52

RESULT 18

US-10-424-599-181420
; Sequence 181420, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 181420
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134837C.1.pep
US-10-424-599-181420

Query Match 89.3%; Score 25; DB 15; Length 57;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 48 HYAMT 52

RESULT 19

US-10-425-115-249920
; Sequence 249920, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 249920
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_159510C.1.pep
US-10-425-115-249920

Query Match 89.3%; Score 25; DB 17; Length 57;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 52 HYAMN 56

RESULT 20

US-10-424-599-177790
; Sequence 177790, Application US/10424599

Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 177790
LENGTH: 58
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(58)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_131560C.1.pep
US-10-424-599-177790

Query Match
Best Local Similarity 89.3%; Score 25; DB 15; Length 58;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 19 HYSMS 23

RESULT 21
US-10-335-977-8261
Sequence 8261, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandasouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8261:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...58
SEQUENCE DESCRIPTION: SEQ ID NO: 8261;
US-10-335-977-8261

Query Match
Best Local Similarity 89.3%; Score 25; DB 15; Length 58;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 21 HVALS 25

RESULT 22
US-10-424-599-214263
Sequence 214263, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 214263
LENGTH: 70
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_35506C.1.pep
US-10-424-599-214263

Query Match
Best Local Similarity 89.3%; Score 25; DB 15; Length 70;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 5 HVALS 9

RESULT 23
US-10-424-599-199143
Sequence 199143, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 199143
LENGTH: 77
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_21850C.1.pep
US-10-424-599-199143

Query Match 89.3%; Score 25; DB 15; Length 77;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 60 HYSMS 64

RESULT 24
US-10-425-115-313005
; Sequence 313005, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 313005
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_48519C.1.pep
US-10-425-115-313005

Query Match 89.3%; Score 25; DB 17; Length 84;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 46 HYAMT 50

RESULT 25
US-10-424-599-275379
; Sequence 275379, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 275379
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(85)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_90688C.1.pep
US-10-424-599-275379

Query Match 89.3%; Score 25; DB 15; Length 85;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 41 HYALS 45

RESULT 26
US-10-424-599-180930
; Sequence 180930, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 180930
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134394C.1.pep
US-10-424-599-180930

Query Match 89.3%; Score 25; DB 15; Length 86;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 15 HYALS 19

RESULT 27
US-10-424-599-231987
; Sequence 231987, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 231987
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(86)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_51506C.1.pep
US-10-424-599-231987

Query Match 89.3%; Score 25; DB 15; Length 86;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 26 HYALS 30

RESULT 28
US-10-424-599-184650
; Sequence 184650, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53222) B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 184650
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_137755C.1.pep
US-10-424-599-184650

Query Match 89.3%; Score 25; DB 15; Length 89;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 37 HYALS 41

RESULT 29
US-10-425-115-270245
; Sequence 270245, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222) B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 270245
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(99)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_17805C.1.pep
US-10-425-115-270245

Query Match 89.3%; Score 25; DB 17; Length 99;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 10 HYALS 14

RESULT 30
US-10-437-963-172988
; Sequence 172988, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221) B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172988
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(100)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71070C.1.pep
US-10-437-963-172988

Query Match 89.3%; Score 25; DB 16; Length 100;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 84 HYSMS 88

RESULT 31
US-10-437-963-165791
; Sequence 165791, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221) B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 165791
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_64563C.1.pep
US-10-437-963-165791

Query Match 89.3%; Score 25; DB 16; Length 107;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 69 HYAMT 73

RESULT 32
US-10-282-122A-77481

```
; Sequence 77481, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77481
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77481

Query Match      89.3%; Score 25; DB 15; Length 126;
Best Local Similarity 80.0%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HYAMS 5
Db      115 HYAMA 119

RESULT 33
US-10-437-963-106924
; Sequence 106924, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
```

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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106924
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11324C.1.pep
US-10-437-963-106924
```

```
Query Match      89.3%; Score 25; DB 16; Length 131;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HYAMS 5
Db      51 HYALS 55
```

```
RESULT 34
US-10-425-115-360208
; Sequence 360208, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 360208
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_91685C.1.pep
US-10-425-115-360208

Query Match      89.3%; Score 25; DB 17; Length 131;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HYAMS 5
Db      78 HYAMA 82

RESULT 35
US-10-424-599-207366
; Sequence 207366, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207366
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
```


LOCATION: (1)..(135)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_29277C.1.pep
US-10-424-599-207366

Query Match 89.3%; Score 25; DB 15; Length 135;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 102 HYALS 106

RESULT 36
US-10-424-599-177566
Sequence 177566, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 177566
LENGTH: 136
TYPE: PRT
ORGANISM: Glycine max
FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_131358C.1.pep
US-10-424-599-177566

Query Match 89.3%; Score 25; DB 15; Length 136;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 66 HYAMA 70

RESULT 37
US-10-424-599-188149
Sequence 188149, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 188149
LENGTH: 148
TYPE: PRT
ORGANISM: Glycine max
FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_140912C.1.pep
US-10-424-599-188149

Query Match 89.3%; Score 25; DB 15; Length 148;
Best Local Similarity 80.0%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 70 HYSMS 74

RESULT 38
US-09-764-868-938
Sequence 938, Application US/09764868
Patent No. US2002016871A1
GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 938
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: SITE
LOCATION: (71)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (105)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (109)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-938

Query Match 89.3%; Score 25; DB 9; Length 150;
Best Local Similarity 80.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 65 HYALS 69

RESULT 39
US-10-425-115-225898
Sequence 225898, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 225898
LENGTH: 174
TYPE: PRT
ORGANISM: Zee maye
FEATURE:

NAME/KEY: unsure
LOCATION: (1)..(174)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_13760C.1.pep
US-10-425-115-225898

Query Match 89.3%; Score 25; DB 17; Length 174;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYAMS 5
 ||||:
 Db 123 HYAMT 127

RESULT 40
 US-10-275-589-3
 ; Sequence 3, Application US/10275589
 ; Publication No. US20040023864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dubois-Stringfellow, Nathalie
 ; APPLICANT: Steve, Rocznik
 ; APPLICANT: Zolotarev, Alya
 ; TITLE OF INVENTION: Method of Regulating Angiogenesis Using RYK Protein
 ; FILE REFERENCE: MSB 7266
 ; CURRENT APPLICATION NUMBER: US/10/275,589
 ; CURRENT FILING DATE: 2002-11-06
 ; PRIOR APPLICATION NUMBER: US 09/568,783
 ; PRIOR FILING DATE: 2000-05-11
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 3
 ; LENGTH: 180
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 ; US-10-275-589-3

Query Match 89.3%; Score 25; DB 15; Length 180;
 Best Local Similarity 80.0%; Pred. No. 8.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
 ||||:
 Db 77 HYALS 81

Search completed: December 17, 2004, 18:37:57
 Job time : 10.6629 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 17, 2004, 18:11:22 ; Search time 1.96629 Seconds
(without alignments)
244665 Million cell updates/sec

Title: US-10-089-500-3

Perfect score: 28

Sequence: 1 HYAMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	119	2	E89999
2	28	100.0	143	2	A71051
3	28	100.0	146	2	AD3630
4	28	100.0	185	2	T37007
5	28	100.0	280	2	E75216
6	28	100.0	280	2	C71453
7	28	100.0	284	2	C72320
8	28	100.0	286	2	A64317
9	28	100.0	288	2	A70371
10	28	100.0	291	2	H69356
11	28	100.0	292	2	F64486
12	28	100.0	295	2	H72529
13	28	100.0	297	2	AB2384
14	28	100.0	424	2	C83159
15	28	100.0	839	2	S62963
16	25	89.3	126	2	U10090
17	25	89.3	216	2	F18072
18	25	89.3	221	2	S69682
19	25	89.3	273	2	C82182
20	25	89.3	283	2	T15932
21	25	89.3	287	2	T22325
22	25	89.3	287	2	T22325
23	25	89.3	310	2	T43158
24	25	89.3	312	2	H89884
25	25	89.3	313	2	T23675
26	25	89.3	314	2	T43299
27	25	89.3	324	2	T50249
28	25	89.3	325	2	A86202
29	25	89.3	333	2	S15238

30	25	89.3	338	2	E75301	conserved hypothet
31	25	89.3	352	1	BVECHD	molybdenum transpo
32	25	89.3	352	2	AE0595	molybdenum transpo
33	25	89.3	352	2	B85579	ATP-binding compo
34	25	89.3	352	2	A90728	ATP-binding compo
35	25	89.3	359	2	AB0844	membrane-bound l
36	25	89.3	361	2	F91073	membrane-bound l
37	25	89.3	361	2	B85918	membrane-bound l
38	25	89.3	361	2	A65050	membrane-bound l
39	25	89.3	367	2	H83088	membrane-bound l
40	25	89.3	394	2	AB1068	probable membrane
41	25	89.3	399	2	F87356	hypothetical prote
42	25	89.3	406	2	G85775	selenocysteine lya
43	25	89.3	406	2	C90927	selenocysteine lya
44	25	89.3	406	2	H64925	aminotransferase n
45	25	89.3	420	2	B87201	hypothetical prote

ALIGNMENTS

RESULT 1

E89999 holo-ACP synthase [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: E89999

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, M.; A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I.

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; PMID:21311952; PMID:11418146

A/Accession: E89999

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-119 <R>

A/Cross-references: UNIPROT:Q99S14; GB:BA000018; PID:G13701866; PIDN:BA843158.1; GSPDB:G

A/Experimental source: strain N315

C/Genetics:

A/Gene: dcpJ

C/Superfamily: holo-ACP synthase

Query Match 100.0%; Score 28; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

Db 106 HYAMS 110

RESULT 2

A71051 hypothetcal protein PH104 - Pyrococcus horikoshii

C/Species: Pyrococcus horikoshii

C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004

C/Accession: A71051

R.; Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohtsuka, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Oguchi, M.;

DNA Res. 5, 55-76, 1998

A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A/Reference number: A71000; PMID:98344137; PMID:9679194

A/Accession: A71051

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-143 <R>

A/Cross-references: UNIPROT:O58831; GB:AP000005; NID:G3236132; PIDN:BA830203.1; PID:G325;

A/Experimental source: strain OT3

A/Note: this accession replaces an interim accession for a sequence replaced by GenBank

C/Genetics:

A/Gene: PH104

Query Match 100.0%; Score 28; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 128 HYAMS 132

RESULT 3
AD3630
pseudozurin [imported] - Brucella melitensis (strain 16M)
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C/Accession: AD3630
R:/DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R.; Mazur, M.; Goldman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leteski, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A/Reference number: AD3252; PMID:11756688
A/Accession: AD3630
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-146 <R>
A/Cross-references: UNIPROT:Q8YB5; GB:AE008918; PIDN:AAU54207.1; PID:917985176; GSPDB:C
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BMEI10965
A/Map position: II
C/Superfamily: plastocyanin

Query Match 100.0%; Score 28; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 104 HYAMS 108

RESULT 4
T37007
probable aminoglycoside nucleotidyltransferase - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T37007
R:/Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999
A/Reference number: Z21618
A/Accession: T37007
A/Status: preliminary; translated from GB/EMBL/DDBA
A/Molecule type: DNA
A/Residues: 1-185 <OLI>
A/Cross-references: UNIPROT:Q9RI70; EMBL:AL109949; PIDN:CAB52921.1; GSPDB:GN00070; SCOP
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: SCODEB:SCU11.36c

Query Match 100.0%; Score 28; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 14 HYAMS 18

RESULT 5
E75216
hypothetical protein PAB2437 - Pyrococcus abyssi (strain Orsay)
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: E75216

R/anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A/Reference number: A75001
A/Accession: E75216
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-280 <RAM>
A/Cross-references: UNIPROT:Q9V218; GB:AJ248283; GB:AL096836; NID:95457433; PIDN:CAB4918(
A/Experimental source: strain Orsay
C/Genetics:
A/Gene: PAB2437
C/Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 126 HYAMS 130

RESULT 6
C71453
hypothetical protein PH0282 - Pyrococcus horikoshii
C/Species: Pyrococcus horikoshii
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C/Accession: C71453
R:/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic ar
A/Reference number: A71000; NID:98344137; PMID:9679194
A/Accession: C71453
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-280 <RAM>
A/Cross-references: UNIPROT:O58020; GB:AP000001; NID:G3236128; PIDN:BAA29354.1; PID:G325(
A/Experimental source: strain OT3
A/Note: this accession replaces an interim accession for a sequence replaced by Genbank
C/Genetics:
A/Gene: PH0282

Query Match 100.0%; Score 28; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 126 HYAMS 130

RESULT 7
C72320
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: C72320
R:/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M. Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; NID:99287316; PMID:10360571
A/Accession: C72320
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-284 <ARN>
A/Cross-references: UNIPROT:Q9X018; GB:AE001755; GB:AE000512; NID:94981432; PIDN:ADJ3599
A/Experimental source: strain MSB8
C/Genetics:
A/Gene: TM0916

C:Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
Db 125 HYAMS 129

RESULT 8

A4317
hypothetical protein M0137 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: A64317
R:Blut, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klank, H.P.; Fraser, C.M.; Smith, H.O.; Moese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; M01D:96337999; PMID:868087
A:Accession: A64317
A:Molecule type: DNA
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Cross-references: UNIPROT:Q57601; GB:U67471; GB:L77117; NID:g2626249; PIDN:AB98120.1;
C:Genetics:
A:Map position: REV134976-134116
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
Db 131 HYAMS 135

RESULT 9

A70371
conserved hypothetical protein seq_814 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: A70371
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V. Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; M01D:98196866; PMID:9537320
A:Accession: A70371
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-288 <NOF>
A:Cross-references: UNIPROT:Q66996; GB:AE000708; NID:g2983356; PIDN:AA06959.1; PID:g298
A:Experimental source: strain VFS
C:Genetics:
A:Gene: seq_814
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
Db 128 HYAMS 132

RESULT 10

H69356
conserved hypothetical protein AF0856 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: H69356
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Kerchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A:Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Moese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
A:Reference number: A69250; M01D:98049343; PMID:9389475
A:Accession: H69356
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-291 <KLE>
A:Cross-references: UNIPROT:Q29403; GB:AE001045; GB:AE000782; NID:g2689368; PIDN:AB9038;
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
Db 134 HYAMS 138

RESULT 11

F64486
hypothetical protein M01495 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: F64486
R:Blut, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klank, H.P.; Fraser, C.M.; Smith, H.O.; Moese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; M01D:96337999; PMID:868087
A:Accession: F64486
A:Molecule type: DNA
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Cross-references: UNIPROT:Q58890; GB:U67590; GB:L77117; NID:g1592126; PIDN:AB99506.1;
C:Genetics:
A:Map position: FOR1468504-1469382
A:Start codon: GTG
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
Db 135 HYAMS 139

RESULT 12

H72529
hypothetical protein APE2212 - Aeropyrum pernix (strain KL)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H72529
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K. DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A:Reference number: A72450; M01D:99310339; PMID:10382966
A:Accession: H72529

A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-295 <XAM>
A/Cross-references: UNIPROT:Q9Y9S6; DDBJ:AF000063; NID:95105654; PIDN:BAAB1224.1; PID:95
A/Experimental source: strain KI
C/Genetics:
A/Gene: APE2212
C/Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 129 HYAMS 133

RESULT 13
AB2284
hypothetical protein alr3825 [imported] - Nostoc sp. (strain PCC 7120)
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AB2284
R/Kanehiko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AB2284
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-297 <KUR>
A/Cross-references: UNIPROT:Q8Y0J8; GB:BA000019; PIDN:BAE75524.1; PID:G17132959; GSPDB:C
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alr3825
C/Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 122 HYAMS 126

RESULT 14
C83159
Na+/H+ antiporter Nhap PA3887 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: C83159
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Micooguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: AB2950; MUID:20437337; PMID:10984043
A/Accession: C83159
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-424 <STO>
A/Cross-references: UNIPROT:O82871; GB:AE004806; GB:AE004091; NID:99550067; PIDN:AA0727
A/Experimental source: strain PA01
C/Genetics:
A/Gene: nhap; PA3887
C/Superfamily: hypothetical protein MJ0057

Query Match 100.0%; Score 28; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 56;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 272 HYAMS 276

RESULT 15
S62963
hypothetical protein YNL041C - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein N2675
C/Species: Saccharomyces cerevisiae
C/Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C/Accession: S62963
R/Duesterhoef, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, April 1996
A/Reference number: S62944
A/Accession: S62963
A/Molecule type: DNA
A/Residues: 1-839 <DUE>
A/Cross-references: UNIPROT:P53959; EMBL:Z71317; NID:G1301893; PID:E239673; PID:G1301894,
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:TF12; MIPS:YNL041C
A/Cross-references: SGD:S0004986
A/Map position: 14L

Query Match 100.0%; Score 28; DB 2; Length 839;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 78 HYAMS 82

RESULT 16
F82072
holo-(acyl-carrier-protein) synthase VC2457 [imported] - Vibrio cholerae (strain N16961 &
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: F82072
R/Haidlberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragol, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: AB2035; MUID:20406833; PMID:10952301
A/Accession: F82072
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-126 <HEI>
A/Cross-references: UNIPROT:Q9KPB6; GB:AE004316; GB:AE003852; NID:9657034; PIDN:AF9559;
A/Experimental source: serogroup O1, strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC2457
A/Map position: 1
C/Superfamily: holo-ACP synthase

Query Match 89.3%; Score 25; DB 2; Length 126;
Best Local Similarity 80.0%; Pred. No. 77;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 115 HYAMA 119

RESULT 17
J10090
ependymin precursor - goldfish
N/Alternate names: preproependymin
C/Species: Carassius auratus (goldfish)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: J10090; PS0306; I51378
R/Koenigsreiter, A.; Steiner, S.; Eckerkorn, C.; Lottspeich, F.; Schmidt, R.; Hoffmann, J. Neurochem. 52, 310-312, 1989
A>Title: Molecular characterization of an ependymin precursor from goldfish brain.
A/Reference number: J10090; MUID:89068004; PMID:2908890
A/Accession: J10090
A/Molecule type: mRNA
A/Residues: 1-216 <KOE>
A/Cross-references: UNIPROT:P13506; GB:X14134; NID:g66577; PIDN:CAA32352.1; PID:g62578
A/Experimental source: brain
A/Accession: PS0306
A/Molecule type: protein
A/Residues: 22-27, 'x', 29-45, 110-123 <KO2>
A/Note: Ependymins beta and gamma have the same amino-terminal sequence
A/Note: 24-Asp, 29-Glu, and 34-Ile were also found
R/Adams, D.S.; Shaatou, V.E.
Gene 141, 237-241, 1994
A/Title: Cloning and sequencing the genes encoding goldfish and carp ependymin.
A/Reference number: I51377; MUID:94215910; PMID:8163195
A/Accession: I51378
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 2-216 <ADA>
A/Cross-references: EMBL:U00433; NID:g397657; PIDN:AAA19566.1; PID:g397658
C/Comment: Ependymins beta and gamma are nervous-system specific glycoproteins localized
C/Comment: These proteins are reported as brain proteins that display enhanced turnover
C/Comment: Ependymin forms dimer with intermolecular disulfide bonds.
A/Genetics:
A/Gene: epn
A/Introns: 29/1; 40/3; 85/3; 148/1; 176/2
C/Superfamily: ependymin
C/Keywords: calcium binding; cell adhesion; glycoprotein
F.1-21/Domain: signal sequence #status predicted <SIG>
F.22-216/Product: ependymin #status experimental <MAT>
F.172,95/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.181,183,185,186/Binding site: calcium (Glu, Glu, Asp, Asp) #status predicted
F.202,203,206,207/Binding site: calcium (Glu, Glu, Asp, Asp) #status predicted

Query Match 89.3%; Score 25; DB 2; Length 216;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
Db 149 HYAMS 153

RESULT 18
S69682
hypothetical protein YDR399W - yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C/Accession: S69682
R/Dietrich, F.S.
submitted to the EMBL Data Library, July 1995
A/Description: The sequence of S. cerevisiae cosmid 9481, 9509, 9926, 9461, and lambda
A/Reference number: S69682
A/Accession: S69682
A/Molecule type: DNA
A/Residues: 1-221 <DIE>
A/Cross-references: UNIPROT:Q04178; EMBL:U32274; NID:g927313; PID:g927331; GSPDB:GN00004
C/Genetics:
A/Gene: SGD:HPT1; MIPS:YDR399W
A/Cross-references: SGD:S0002807
A/Map position: 4R
C/Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC23C11.13c

Query Match 89.3%; Score 25; DB 2; Length 221;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5

Db 120 HYALS 124

RESULT 19
C82182
hypothetical protein VC1577 [imported] - vibrio cholerae (strain N16961 serogroup O1)
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: C82182
R/Haidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gilm, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bae, S.; Qin, H.; Dragoi, I.; Sellers, P. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: C82182
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-273 <HEI>
A/Cross-references: UNIPROT:Q9KR09; GB:AE004235; GB:AE003852; NID:g9656082; PIDN:AAF9473;
A/Experimental source: serogroup O1, strain N16961, biotype El Tor
C/Genetics:
A/Gene: VC1577
A/Map position: 1

Query Match 89.3%; Score 25; DB 2; Length 273;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
Db 215 HYALS 219

RESULT 20
T15932
hypothetical protein EGAP2.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15932
R/Bentley, D.
submitted to the EMBL Data Library, December 1995
A/Description: The sequence of C. elegans cosmid EGAP2.
A/Reference number: Z16430
A/Accession: T15932
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-283 <BEN>
C/Genetics:
A/Gene: CESP:EGAP2.1
A/Introns: 97/2; 164/1; 214/2

Query Match 89.3%; Score 25; DB 2; Length 283;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYAMS 5
Db 16 HYALS 20

RESULT 21
T22325
hypothetical protein F46G10.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22325
R/Coles, L.
submitted to the EMBL Data Library, July 1995
A/Reference number: Z19548
A/Accession: T22325

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-287 <WIL>
A:Cross-references: UNIPROT:Q20481; EMBL:Z50177; PIDN:CAA90547.1; GSPDB:GN00028; CESP:F4
A:Experimental source: clone F46G10
C:Genetics:
A:Gene: CESP:F46G10.3
A:Map position: X
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Superfamily: conserved hypothetical protein b1120

Query Match 89.3%; Score 25; DB 2; Length 287;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 98 HYALS 102

RESULT 22

T22324
hypothetical protein F46G10.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22324
R:Colles, L.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z19548

A:Accession: T22324
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-287 <WIL>

A:Cross-references: UNIPROT:Q20480; EMBL:Z50177; PIDN:CAA90546.1; GSPDB:GN00028; CESP:F4
A:Experimental source: clone F46G10
C:Genetics:
A:Gene: CESP:F46G10.7
A:Map position: X
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 16-Aug-2004
C:Superfamily: conserved hypothetical protein b1120

Query Match 89.3%; Score 25; DB 2; Length 287;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 98 HYALS 102

RESULT 23

T43158
probable GMP-binding protein beta chain - fission yeast (Schizosaccharomyces pombe) (fr

C:Species: Schizosaccharomyces pombe
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 16-Aug-2004
C:Accession: T43158
R:Yoshioaka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997

A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:9816722; PMID:9501991
A:Accession: T43158
A:Map position: X

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-310 <YOS>

A:Cross-references: EMBL:D89247; NID:G1749701; PIDN:BAAL3908.1; PID:G1749702
A:Experimental source: strain PR745
C:Superfamily: WD repeat homology
C:Keywords: GMP binding

Query Match 89.3%; Score 25; DB 2; Length 310;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 72 HYALS 76

RESULT 24

H89884
hypothetical protein SA0987 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H89884

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani, U.; I.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; i
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirata, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89884
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-312 <KUR>
A:Cross-references: UNIPROT:Q99UM5; GB:BA000018; PID:G13700940; PIDN:BA042236.1; GSPDB:G
C:Experimental source: strain N315
C:Genetics:
A:Gene: SA0987

Query Match 89.3%; Score 25; DB 2; Length 312;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 216 HYALS 220

RESULT 25

T23675
hypothetical protein M02B1.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23675
R:Lightning, J.
submitted to the EMBL Data Library, October 1996

A:Reference number: Z19780
A:Accession: T23675
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-313 <WIL>
A:Cross-references: UNIPROT:Q93893; EMBL:Z81102; PIDN:CA003203.1; GSPDB:GN00022; CESP:M0
A:Experimental source: clone M02B1
C:Genetics:
A:Gene: CESP:M02B1.4
A:Map position: 4
A:Intons: 31/2; 195/3; 228/1

Query Match 89.3%; Score 25; DB 2; Length 313;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 173 HYALS 177

RESULT 26

T43299
probable GTP-binding regulatory protein beta chain - fission yeast (Schizosaccharomyces f

N;Alternate names: guanine nucleotide regulatory protein
C:Species: Schizosaccharomyces pombe
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 16-Aug-2004
C:Accession: T43299; T39022
R:Park, S.K.; Yoo, H.S.
unpublished results 1994, cited by EMBL

A:Reference number: 222403
A:Accession: T43239
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-314 <PAR>
A:Cross-references: UNIPROT:Q10281; EMBL:L37885; PIDN:AAA56865.1
A:Experimental source: isolate ED616
R:Gentile, S.; Churchill, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, August 1995
A:Reference number: 221815
A:Accession: T39022
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-314 <GEN>
A:Cross-references: EMBL:Z98531; PIDN:CAH11079.1; GSDDB:GN00066; SPDB:SPAC6B12.15
A:Experimental source: strain 972h-; comid c6B12
C:Genetics:
A:Gene: SPAC6B12.15
A:Map position: 1
A:introns: 42/3; 175/3
C:Superfamily: WD repeat homology
C:keywords: GTP binding

	Query Match	89.3%;	Score 25;	DB 2;	Length 31d;
	Best Local Similarity	80.0%;	Pred. No. 2e+02;		
	Matches	4;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0;
OY	1 HYAMS	5			
		4:			
Db	76 HYALS	80			

RESULT 27
 T50249
 conserved hypothetical protein SPAC694.04c [imported] - fission yeast (*Schizosaccharomyces*
C. Species: Schizosaccharomyces pombe
C. Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C. Accession: T50249
R. Part: R. Volckert, G. McDougall, R. C. Rajandream, M. A. Barrell, B. G.
submitted to the EMBL Data Library, February 2000
A. Reference number: Z25049
A. Accession: T50249
A. Status: preliminary; translated from GB/EMBL/DBJ
A. Molecule type: DNA
A. Features: 1-324 <AER>
A. Cross-references: UNIPROT:Q9PTT6, EMBL:ALJ38666; PIDD: CAB71842.1; GSPDB:GN00066; SPDB:
A. Experimental source: strain 972h(-); cosmid c694
C. Genes:
A. Gene: SPDB:SPAC694.04c
A. Map position: 1
A. Introns: 19/1
C. Superfamily: Arbidopsis thaliana hypothetical protein F2K15.180

Query Match	89.3%	Score 25	DB 2	Length 324
Best Local Similarity	80.0%	Pred. No. 2.1e+02		
Matches	4	Conservative	1	Mismatches 0
				Indels 0
				Gaps 0
QY	1	HYAMS	5	
Db	193	HYALS	197	

RESULT 28
 A86202
 hypothetical protein [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear crease)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: A86202
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

Citro, A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Matci, R.; Marzall, R.Z.; M., Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:1130712
A:Accession: A86202
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <STO>
A:Cross-references: UNIPROT:Q9M9Y1; GB:AE005172; NID:G523706; PIDN:AAE63145.1; GSPDB:GNC
C:Genetics:
A:Map position: 1

```

Query Match      89.3%; Score 25; DB 2; Length 355;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY      1 HYAMS 5
        |||:-|
Db       16 HYALS 20

```

RESULT 29
S15238
O-antigen acetylase (EC 2.3.1.-) - enterobacterial phage Sf6
N/Alternate names: acetyl transferase
C/Species: enterobacterial phage Sf6
C/Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #ext_change 15-Oct-1999
C/Accession: S15238; J50588; S24220
R/Verma, N.K.; Brandt, J.M.; Verma, D.J.; Lindberg, A.A.
Mol. Microbiol. 5, 71-75, 1991
A>Title: Microbial characterization of the O-acetyl transferase gene of converting bacteria
A/Reference number: S15238; MUID:91194560; PMID:2014005
A/Accession: S15238
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333 <VER>
A/Cross-references: EMBL:X56800; NID:g14867; PIDN:CMA40136.1; PID:g14868
R/Clark, C.A.; Beltz, J.; Manning, P.A.
Gene 107, 43-52, 1991
A>Title: The oac gene encoding a lipopolysaccharide O-antigen acetylase maps adjacent to
A/Reference number: J50587; MUID:92077435; PMID:1720755
A/Accession: J50588
A/Molecule type: DNA
A/Residues: 1-157, 'L', 159-168, 'Q', 170-333 <CLA>
A/Cross-references: EMBL:X59553; NID:g15748; PID:g15750
C/Comment: This enzyme catalyzes O-acetylation of the O-antigen of the lipopolysaccharide
C/genetics:
A/Name: oac
A/Keywords: acyltransferase

Query Match	89.3%;	Score 25;	DB 2;	Length 333;
Best Local Similarity	80.0%;	Pred. No. 2.2e+02;		
Matches	4;	Conservative	0;	Mismatches 0;
				Indels
Oy	1	HYAMS	5	
Db	23	HYALS	27	

RESULT 30
E75301
conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ext_change 03-Nov-2003
C:Accession: E75301
R:White, O.; Eksen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uetrecher, T.; Zalewski, C.; Mat
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radiation-resistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: E75301
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-338 <WHI>
A/Cross-references: GB:AE002054; GB:AE000513; NID:g6460010; PIDN:AAFI1759.1; PID:g646001
A/Experimental source: strain RI
C/Genetics:
A/Genes: DR2213
A/Map position: 1
C/Superfamily: uncharacterized conserved protein

Query Match 89.3%; Score 25; DB 2; Length 338;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 260 HYAMS 264

RESULT 31
BVECHD
molybdenum transport protein modC - Escherichia coli (strain K-12)
N/Alternate names: molybdenum transport protein chld
C/Species: Escherichia coli
C/Date: 31-Dec-1990 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
C/Accession: B64812; B26871
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; WUID:9742617; PMID:9278503
A/Accession: B64812
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-352 <BLAT>
A/Cross-references: UNIPROT:P09833; GB:AE000179; GB:U00096; NID:g1786378; PIDN:AACT3852.
A/Experimental source: strain K-12, substrain MG1655
R/Johnson, S.; Hinton, S.M.
J. Bacteriol. 169, 1911-1916, 1987
A/Title: Cloning and nucleotide sequence of the chld locus.
A/Reference number: A26871; WUID:87194564; PMID:3553151
A/Accession: B26871
A/Molecule type: DNA
A/Residues: 1-243; 'SALRDDR', 251-268, 'LRRYPHSGFRCSMFYNNRSGP', 269, 'FVT', 273, 'AGKSC' <JOH>
A/Cross-references: EMBL:X07875
A/Experimental source: strain K12
A/Note: the authors translated the codon GAA for residue 74 as Gly
C/Genetics:
A/Genes: modC; chld
A/Map position: 17 min
C/Function:
A/Description: nucleotide-binding protein component of the binding protein-dependent tra
C/Superfamily: molybdenum transport protein modC; ATP-binding cassette homology
C/Keywords: ATP; inner membrane; molybdenum transport; nucleotide binding; P-loop
F/14-205/Domain: ATP-binding cassette homology <ABC>
F/31-38/Region: nucleotide-binding motif A (P-loop)
F/149-153/Region: nucleotide-binding motif B

Query Match 89.3%; Score 25; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 245 HYAMT 249

RESULT 32
AE0595
molybdenum transport ATP-binding protein modC STY0816 [imported] - Salmonella enterica s
C/Species: Salmonella enterica subsp. enterica serovar typhi
A/Note: this species has also been called Salmonella typhi

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Nov-2002
C/Accession: AE0595
C/Species: Escherichia coli
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; WUID:21534947; PMID:11677608
A/Accession: AE0595
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-352 <PAR>
A/Cross-references: GB:AL51382; PIDN:CAD05231.1; PID:g16502001; GSPDB:GN00176
C/Genetics:
A/Genes: STY0816
C/Superfamily: molybdenum transport protein modC; ATP-binding cassette homology

Query Match 89.3%; Score 25; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 245 HYAMT 249

RESULT 33
B85579
ATP-binding component of molybdate transport [imported] - Escherichia coli (strain O157:H7)
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: B85579
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Illier, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; WUID:21074935; PMID:11206551
A/Accession: B85579
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-352 <STO>
A/Cross-references: UNIPROT:Q8X4V7; GB:AE005174; NID:g12513697; PIDN:AAG55094.1; GSPDB:GT
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Genes: modC
C/Superfamily: molybdenum transport protein modC; ATP-binding cassette homology

Query Match 89.3%; Score 25; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
|||||
DB 245 HYAMT 249

RESULT 34
A90728
ATP-binding component of molybdate transport [imported] - Escherichia coli (strain O157:H7)
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: A90728
R/Hayashi, T.; Makino, K.; Ohishi, M.; Kurokawa, K.; Ichii, K.; Yokoyama, K.; Han, C.G.;
gaewara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A/Reference number: A99629; WUID:21156231; PMID:11258796
A/Accession: A90728
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-352 <HAY>
A/Cross-references: UNIPROT:Q8X4V7; GB:BA000007; PIDN:BA034216.1; PID:g13360252; GSPDB:GT

A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC60793
C:Superfamily: molybdenum transport protein modC; ATP-binding cassette homology

Query Match 89.3%; Score 25; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 245 HYAMT 249

RESULT 35

AB0844

membrane-bound lytic transglycosylase B precursor (EC 3.2.1.-) [imported] - Salmonella

C:Species: Salmonella enterica subsp. enterica serovar Typhl

A:Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AB0844

R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,

th, T.; Conerton, B.; Croxin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AB0844

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD05937.1; PID:G1503908; GSPDB:GN00176

C:Genetics:

A:Gene: STY2952

C:Keywords: glycosidase; hydrolase

Query Match 89.3%; Score 25; DB 2; Length 359;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 341 HYAMA 345

RESULT 36

membrane-bound lytic murein transglycosylase B EC63558 [imported] - Escherichia coli (str

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: F91073

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasaara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: F91073

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-361 <HAY>

A:Cross-references: UNIPROT:Q8X872; GB:BA000007; PIDN:BA536981.1; PID:G13363029; GSPDB:G

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: EC63558

Query Match 89.3%; Score 25; DB 2; Length 361;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 341 HYAMA 347

RESULT 37

membrane-bound lytic murein transglycosylase B [imported] - Escherichia coli (strain O157

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: B85918

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousie, K.; Apodaca,

Nature 409, 529-533, 2001

A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B85918

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-361 <STO>

A:Cross-references: UNIPROT:Q8X872; GB:AE005174; NID:G12517141; PIDN:AA657806.1; GSPDB:G

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: mltB

Query Match 89.3%; Score 25; DB 2; Length 361;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 343 HYAMA 347

RESULT 38

membrane-bound lytic transglycosylase (EC 3.2.1.-) B precursor - Escherichia coli (strain

N:Alternate names: mltB protein

C:Species: Escherichia coli

C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C:Accession: A65050; S65868; S77642

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

A.; Rose, D.J.; Mau, B.; Shaq, Y.

Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A65050

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-361 <BLAT>

A:Cross-references: UNIPROT:P41052; GB:AE000354; GB:U00096; NID:G2367149; PIDN:AACT5743.3

A:Experimental source: strain K-12, substrain MG1655

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

EBBS Lett. 366, 115-118, 1995

A>Title: Cloning and controlled overexpression of the gene encoding the 35 kDa soluble 1)

A:Reference number: S65868; MUID:95309413; PMID:7789526

A:Accession: S65868

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-334, 'A', 35-361 <DIJ>

R:Phlert, K.; Hoeltje, J.V.; Templin, M.F.

Mol. Microbiol. 16, 761-768, 1995

A>Title: Cloning and expression of a murein hydrolase 11poprotein from Escherichia coli.

A:Reference number: S77642; MUID:96065704; PMID:7476170

A:Accession: S77642

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-361 <EHL>

A:Cross-references: EMBL:U18785; NID:G642537; PIDN:AA60060.1; PID:G642538

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994

C:Genetics:

A:Gene: mltB

C:Keywords: glycosidase; hydrolase

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-361/Product: mltB protein #status predicted <MAT>

Query Match 89.3%; Score 25; DB 2; Length 361;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
 ||||:
 DB 343 HVAMA 347

RESULT 39

H83088
 membrane-bound lytic transglycosylase PA4444 [imported] - Pseudomonas aeruginosa (strain
 C/Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C/Accession: H83088
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.U.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A/Reference number: AB2950; WUID:20437337; PMID:10984043
 A/Accession: H83088
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1367 <STO>
 A/Cross-references: UNIPROT:Q9HVX3; GB:AE004859; GB:AE004091; NID:G9950678; PIDN:AA00783
 A/Experimental source: strain PA01
 C/Genetics:
 A/Gene: mltB1, PA4444

Query Match 89.3%; Score 25; DB 2; Length 367;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
 ||||:
 DB 343 HVAMA 347

RESULT 40

AB1068
 Probable membrane protein STY4872 (imported) - Salmonella enterica subsp. enterica serov
 C/Species: Salmonella enterica subsp. enterica serovar Typh
 A/Note: this species has also been called Salmonella typh
 C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C/Accession: AB1068
 R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 . S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A/Reference number: AB0502; WUID:21534947; PMID:11677608
 A/Accession: AB1068
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-394 <PAR>
 A/Cross-references: GB:AL513382; PIDN:CAD03361.1; PID:G16505633; GSPDB:GN00176
 C/Genetics:
 A/Gene: STY4872

Query Match 89.3%; Score 25; DB 2; Length 394;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
 ||||:
 DB 163 HVALS 167

Search completed: December 17, 2004, 18:30:13
 Job time : 2.96629 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 17, 2004, 18:29:23 ; Search time 14.9438 Seconds
(without alignments)
192.513 Million cell updates/sec

Title: US-10-089-500-3

Perfect score: 28

Sequence: 1 HYAMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_02:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	119	1	ACPS_STAM
2	28	100.0	119	1	ACPS_STAM
3	28	100.0	119	2	Q99614 staphylococ
4	28	100.0	119	2	Q99614 staphylococ
5	28	100.0	143	2	Q99614 staphylococ
6	28	100.0	146	2	Q99614 staphylococ
7	28	100.0	185	2	Q99614 staphylococ
8	28	100.0	274	2	Q99614 staphylococ
9	28	100.0	274	2	Q99614 staphylococ
10	28	100.0	275	2	Q99614 staphylococ
11	28	100.0	275	2	Q99614 staphylococ
12	28	100.0	280	2	Q99614 staphylococ
13	28	100.0	280	2	Q99614 staphylococ
14	28	100.0	280	2	Q99614 staphylococ
15	28	100.0	284	2	Q99614 staphylococ
16	28	100.0	286	2	Q99614 staphylococ
17	28	100.0	288	2	Q99614 staphylococ
18	28	100.0	291	2	Q99614 staphylococ
19	28	100.0	292	2	Q99614 staphylococ
20	28	100.0	292	2	Q99614 staphylococ
21	28	100.0	295	2	Q99614 staphylococ
22	28	100.0	297	2	Q99614 staphylococ
23	28	100.0	345	2	Q99614 staphylococ
24	28	100.0	424	2	Q99614 staphylococ
25	28	100.0	424	2	Q99614 staphylococ
26	28	100.0	448	2	Q99614 staphylococ
27	28	100.0	453	2	Q99614 staphylococ
28	28	100.0	453	2	Q99614 staphylococ
29	28	100.0	464	2	Q99614 staphylococ
30	28	100.0	555	1	NU5M_CANPA
31	28	100.0	839	1	COD2_YEAST

32	28	100.0	1012	2	Q6CHS4	Q6CHS4 yarrowia li
33	28	100.0	1268	1	S24B_HUMAN	Q95487 homo sapien
34	28	100.0	1675	1	Q9VLT1	Q9VLT1 drosophila
35	25	89.3	19	2	Q6CHS4	Q6CHS4 halocynthia
36	25	89.3	56	2	Q6CHS4	Q6CHS4 aeromonas h
37	25	89.3	56	2	Q6CHS4	Q6CHS4 aeromonas h
38	25	89.3	60	2	Q6CHS4	Q6CHS4 aeromonas h
39	25	89.3	98	2	Q6CHS4	Q6CHS4 aeromonas h
40	25	89.3	116	2	Q6CHS4	Q6CHS4 aeromonas h
41	25	89.3	119	2	Q6CHS4	Q6CHS4 aeromonas h
42	25	89.3	119	2	Q6CHS4	Q6CHS4 aeromonas h
43	25	89.3	120	2	Q6CHS4	Q6CHS4 aeromonas h
44	25	89.3	120	2	Q6CHS4	Q6CHS4 aeromonas h
45	25	89.3	126	1	ACPS_VIBCH	Q9XBD6 vibrio chol

ALIGNMENTS

RESULT 1
ACPS_STAM STANDARD; PRT; 119 AA.
ID ACPS_STAM
AC Q99614,
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps)
GN Name=acps, Synonyms=cpj, OrderedLocName=SV2071, SA1875, MM1995;
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain N315), and
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=1418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshino A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano S., Goto S., Yabuzaki J.,
RA Sekizawa K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsuka K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus",
RL Lancet 357:1225-1240(2001).
[2]
RC SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratsuka K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA",
RL Lancet 359:1819-1827(2002).
[3]
AC - FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
A to a Ser of acyl-carrier protein (By similarity).
CC - CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
3',5'-bisphosphate + holo-[acyl-carrier protein].
CC - COFACTOR: Magnesium (By similarity).
CC - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC - SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
family.

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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL; AP003364; BAB58233.1; -.
DR EMBL; AP003364; BAB43158.1; -.
DR EMBL; AP004829; BAB95860.1; -.
DR PIR; E89999; E89999.
DR HSSP; P96618; 1F7L.
DR HAMAP; MF_00101; -.
DR InterPro; IPR008278; 4-PPT_transf.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantethn_trans.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRPFAMs; TIGR00516; acps; 1.
DR TIGRPFAMs; TIGR00556; pantethn_trn; 1.
DR Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KM Magnesium; Transferase.
FT METAL 8 59 Magnesium (By similarity).
FT METAL 59 59 Magnesium (By similarity).
SQ SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 106 HYAMS 110

RESULT 2
ACPS_STRAU STANDARD; PRT; 119 AA.
ID ACPS_STRAU
AC 09ZAH6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; Synonyms=dpj;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
OX NCBI_TaxID=1280;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325;
RX MEDLINE=98434453; PubMed=9756984;
RA Kullik I., Jenni R., Berger-Bachi B.;
RT "Sequence of the putative alanine racemase operon in Staphylococcus
RT aureus: Insertional interruption of this operon reduces D-alanine
RT substitution of lipoic acid and autolysis.";
RL Gene 219;9-17(1998).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC 3',5'-bisphosphate + holo-[acyl-carrier protein] = adenosine
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@lsb-sib.ch).
CC -----
CC EMBL; Y16431; CAA76220.1; -.
DR HSSP; P96618; 1F7L.
DR HAMAP; MF_00101; -.
DR InterPro; IPR008278; 4-PPT_transf.

```

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DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantethn_trans.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRPFAMs; TIGR00516; acps; 1.
DR TIGRPFAMs; TIGR00556; pantethn_trn; 1.
DR Fatty acid biosynthesis; Lipid synthesis; Magnesium; Transferase.
FT METAL 8 59 Magnesium (By similarity).
FT METAL 59 59 Magnesium (By similarity).
SQ SEQUENCE 119 AA; 13605 MW; 0B828A811774B138 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 106 HYAMS 110

RESULT 3
06G7N8 PRELIMINARY; PRT; 119 AA.
ID 06G7N8
AC 06G7N8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7).
GN ORFNames=SAS1976;
OS Staphylococcus aureus subsp. aureus MSSA476.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282459;
OX NCBI_TaxID=282459;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MSSA476;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Erricht M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch B., Rutherford K., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC EMBL; BX571857; CAG43783.1; -.
DR InterPro; IPR008278; 4-PPT_transf.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantethn_trans.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRPFAMs; TIGR00516; acps; 1.
DR TIGRPFAMs; TIGR00556; pantethn_trn; 1.
DR Transferase.
SQ SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 106 HYAMS 110

RESULT 4
06G7N8 PRELIMINARY; PRT; 119 AA.
ID 06G7N8
AC 06G7N8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

```

```
DT 05-JUL-2004 (TEMBLrel. 27, last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7).
GN Name=acps; ORFNames=SA82159;
OS Staphylococcus aureus subsp. aureus MRSA252.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MRSA252;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL: BX571856; CAG41140.1; -.
DR InterPro: IPR008278; 4-PPT_transf.
DR InterPro: IPR002582; ACPS.
DR InterPro: IPR004568; Pantechn_trans.
DR Pfam: PF004282; ACPS; 1.
DR ProDom: PD004282; ACPS; 1.
DR TIGRPFAM: TIGR00516; acps; 1.
DR TIGRPFAM: TIGR00556; pantechn_trn; 1.
KW Transferrase.
SQ SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 106 HYAMS 110

RESULT 5
058831 PRELIMINARY; PRT; 143 AA.
AC 058831;
DT 01-AUG-1998 (TEMBLrel. 07, Created)
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DE Hypothetical protein PH1104.
DE Hypothetical protein PH1104.
GN OrderedLocuNames=PH1104;
OS Pyrococcus horikoshii;
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RA MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kobugi H., Hosoyma A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamitaya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL: AP000005; BAA32023.1; -.
DR PIR: A71051; A71051.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 143 AA; 16220 MW; 48B66A1605A86661 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 143;
```

```
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 128 HYAMS 132

RESULT 6
08YBD5 PRELIMINARY; PRT; 146 AA.
ID 08YBD5;
AC 08YBD5;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DE 01-MAR-2004 (TEMBLrel. 26, last annotation update)
DE PSEUDAZURIN.
GN OrderedLocuNames=BME10965;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=1156688; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Ios T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jabloncki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Bizer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL: AE009729; AAL54207.1; -.
DR PIR: AD3630; AD3630.
DR HSSP: P04377; IPAZ.
DR GO: GO:0005507; F:copper ion binding; IEA.
DR GO: GO:0005489; F:electron transporter activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR002386; Amicyanin.
DR InterPro: IPR000923; BlueCu_1.
DR InterPro: IPR001235; Copper_blue.
DR InterPro: IPR011572; Copper_blue_sub.
DR InterPro: IPR008972; Cupredoxin.
DR Pfam: PF00127; Copper_bind; 1.
DR PRINTS: PR00155; AMICYANIN.
DR PRINTS: PR00156; COPPERBLUE.
DR ProDom: PD001235; Copper_blue_sub; 1.
KW Complete proteome.
SQ SEQUENCE 146 AA; 15897 MW; 36ADAA0FEE6915E6 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 104 HYAMS 108

RESULT 7
09R170 PRELIMINARY; PRT; 185 AA.
ID 09R170;
AC 09R170;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, last annotation update)
DE Putative aminoglycoside nucleotidyltransferase.
GN OrderedLocuNames=SC00107; ORFNames=SCU11.36c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Frazer A., Godle A., Hidalgo J., Hornby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajendram M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL939104; CAB52921.1; -.
DR PIR: T37007; T37007.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR000669; Manitol_dh.
DR PROSITE: PS00974; MANNITOL_DHEXAMASE; UNKNOWN_1.
KM Complete proteome; Transferase.
SQ SEQUENCE 185 AA; 20294 MW; B08AFD1F4B12C31 CRC64;
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Query Match 100.0%; Score 28; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HYAMS 5
DB 14 HYAMS 18
```

RESULT 8

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ID 06M194 PRELIMINARY; PRT; 274 AA.
AC 06M194;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=MMP0023;
OS Methanococcus maripaludis;
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
NCBI_TaxID=39152;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S2 / LL;
RA Hendrickson E.L., Kaul R., Zhou Y., Boyee D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
RA Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
RA Leigh J.A.;
RT "Complete genome sequence of the mesophilic hydrogenotrophic
RT methanogen Methanococcus maripaludis.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX957219; CAF29579.1; -.
DR InterPro: IPR002825; DUF114.
DR Pfam: PF01972; DUF114.1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 274 AA; 31452 MW; E0CD99AD6B8848B9 CRC64;
```

```

Query Match 100.0%; Score 28; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 HYAMS 5
DB 120 HYAMS 124
```

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RESULT 9
ID CAF29579 PRELIMINARY; PRT; 274 AA.
AC CAF29579;
DT 03-MAR-2004 (TrEMBLrel. 27, Created)
DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN MMP0023.
OS Methanococcus maripaludis.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
NCBI_TaxID=39152;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S2 / LL;
RA Hendrickson E.L., Kaul R., Zhou Y., Boyee D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
RA Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
RA Leigh J.A.;
RT "Complete genome sequence of the mesophilic hydrogenotrophic
RT methanogen Methanococcus maripaludis.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX957219; CAF29579.1; -.
KM Hypothetical protein.
SQ SEQUENCE 274 AA; 31452 MW; E0CD99AD6B8848B9 CRC64;
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```

Query Match 100.0%; Score 28; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HYAMS 5
DB 120 HYAMS 124
```

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RESULT 10
ID 0721M1 PRELIMINARY; PRT; 275 AA.
AC 0721M1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Periplasmic serine protease.
GN OrderedLocuNames=TTCl111;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15064768;
RX Heine A., Brueggemann H., Raasch C., Wierzer A., Hartisch T.,
RX Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RX Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RX Klensk H.-P., Kramar W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus.";
RL Nat. Biotechnol. 22:547-553(2004).
DR EMBL: AE017304; AAS81453.1; -.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR InterPro: IPR002825; DUF114.
DR Pfam: PF01972; DUF114.1.
KM Complete proteome; Protease.
SQ SEQUENCE 275 AA; 31051 MW; EF05B9130D12FEF2 CRC64;
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Query Match 100.0%; Score 28; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1 HYAMS 5
```


Db 121 HYAMS 125

RESULT 11

AA581453 PRELIMINARY; PRT; 275 AA.

AC AAS81453; (T-EMBLrel. 27, Created)
 DT 14-APR-2004 (T-EMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (T-EMBLrel. 27, Last sequence update)
 DE Periplasmic serine protease.
 GN TTC111.
 OS *Thermus thermophilus* (strain HB27 / ATCC BAA-163 / DSM 7039).
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC *Thermus*.
 NC NCB1_TaxID=262724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15064768;
 RA Henne A., Bruggemann H., Raasch C., Wierer A., Hartsch T.,
 RA Joesang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
 RA Jacob C., Starkuvienė V., Schlenker S., Dencker S., Huber R.,
 RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Filtz H.-G.,
 RA "The genome sequence of the extreme thermophile *Thermus*
 RT *thermophilus*."
 RL Nat. Biotechnol. 22:547-553(2004).
 DR EMBL; AE017304; AAS81453.1; .
 KW PROTEASE.
 SQ SEQUENCE 275 AA; 31051 MW; EF05B9130D12FEF2 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 275;

Best Local Similarity 100.0%; Pred. No. 2, 1e+02; Mismatches 0; Gaps 0;

Qy 1 HYAMS 5
 Db 121 HYAMS 125

RESULT 12

OS8020 PRELIMINARY; PRT; 280 AA.

AC OS8020; (T-EMBLrel. 07, Created)
 DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
 DT 01-AUG-1998 (T-EMBLrel. 24, Last annotation update)
 DE Hypothetical protein PH0282.
 GN OrderedLocustNames=PH0282;
 OS *Pyrococcus horikoshii*.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC *Pyrococcus*.
 NC NCB1_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kobugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.";
 RL DNA Res. 5:55-76(1998).
 DR EMBL; AP000001; BAA29354.1; .
 DR PIR; C71453; C71453.
 DR InterPro; IPR002825; DUF114.
 DR Pfam; PF01972; DUF114; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 280 AA; 31784 MW; 6ABD616BD465D375 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2, 2e+02; Mismatches 0; Gaps 0;

Qy 1 HYAMS 5
 Db 126 HYAMS 130

RESULT 13

Q9V218 PRELIMINARY; PRT; 280 AA.

AC Q9V218; (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (T-EMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=PYRAB02560; ORFNames=PAE2437;
 OS *Pyrococcus abyssi*.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC *Pyrococcus*.
 NC NCB1_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=GB5 / Orsay;
 RA Cohen G.N., Barbe V., Flament D., Galperin M., Hellig R., Lecompte O.,
 RA Poch O., Prieur D., Querellou J., Ripp R., Thiery J.-C.,
 RA Van der Oost J., Weisenbach J., Zivanovic Y., Forterre P.,
 RA "An integrated analysis of the genome of the hyperthermophilic
 RT archaeon *Pyrococcus abyssi*."
 RL Mol. Microbiol. 47:1495-1512(2003).
 DR EMBL; AJ248283; CAB49180.1; .
 DR PIR; E75216; E75216.
 DR InterPro; IPR002825; DUF114.
 DR Pfam; PF01972; DUF114; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 280 AA; 31874 MW; 04DA906328363177 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 280;

Best Local Similarity 100.0%; Pred. No. 2, 2e+02; Mismatches 0; Gaps 0;

Qy 1 HYAMS 5
 Db 126 HYAMS 130

RESULT 14

Q8U454 PRELIMINARY; PRT; 280 AA.

AC Q8U454; (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Hypothetical protein PF0240.
 GN OrderedLocustNames=PF0240;
 OS *Pyrococcus furiosus*.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC *Pyrococcus*.
 NC NCB1_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 3638;
 RX MEDLINE=21079003; PubMed=11210495;
 RA Robb F.T., Maeder D.L., Brown J.R., DiRuggiero J., Stump M.D.,
 RA Yeh R.K., Weiss R.B., Dunn D.M.;
 RT "Genomic sequence of hyperthermophile, *Pyrococcus furiosus*;
 RT implications for physiology and enzymology.";
 RL Meth. Enzymol. 330:134-157(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;

```

RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010149; AAL80364.1; -.
DR InterPro: IPR002825; DUF114.
DR Pfam; PF01972; DUF114.1.
SQ Complete proteome; Hypothetical protein.
KW SEQUENCE 280 AA; 31627 MW; 451EFAA1057C4579 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 126 HYAMS 130

RESULT 15
ID Q9X018 PRELIMINARY; PRT; 284 AA.
AC Q9X018;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedlocusNames=TM0916;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=3336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Sutton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima."
RL Nature 399:323-329 (1999).
DR EMBL; AE001755; AAD35997.1; -.
DR PIR; C72320; C72320.
DR TIGR; TM0916; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR002825; DUF114.
DR InterPro: IPR002142; Peptidase_S49.
DR Pfam; PF01972; DUF114.1.
DR ProDom; PD002897; Peptidase_S49; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 284 AA; 32142 MW; 2D0B0D47CDF66121 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 125 HYAMS 129

RESULT 16
ID Y137_METUA STANDARD; PRT; 286 AA.
AC Y137_METUA
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein MJ0137.
GN OrderedlocusNames=MJ0137;

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OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake O., Olsen G.J., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073 (1996).
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CC CC
DR EMBL; U67471; AAB98120.1; -.
DR PIR; A6317; A6317.
DR TIGR; MJ0137; -.
DR InterPro: IPR002825; DUF114.
DR Pfam; PF01972; DUF114.1.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 8 38
SQ SEQUENCE 286 AA; 32166 MW; A43DD345B569C5F CRC64;

Query Match 100.0%; Score 28; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 131 HYAMS 135

RESULT 17
ID O66996 PRELIMINARY; PRT; 288 AA.
AC O66996;
DT 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein aq_814.
GN OrderedlocusNames=AQ_814;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358 (1998).
DR EMBL; AE000708; AAC06959.1; -.
DR PIR; A70371; A70371.
DR InterPro: IPR002825; DUF114.
DR Pfam; PF01972; DUF114.1.

```

KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 288 AA; 32624 MW; 3D86253B32AF730 CRC64;
 Query Match 100.0%; Score 28; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
 Db 128 HYAMS 132

RESULT 18
 ID 029403 PRELIMINARY; PRT; 291 AA.
 AC 029403;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DE Hypothetical protein AF0856.
 DE Hypothetical protein AF0856.
 GN OrderedlocusNames=AF0856;
 OS Archaeoglobus fulgidus.
 OC Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 NCBI_TaxID=2234;
 RN NCBI_TaxID=2234;
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyriades N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,
 RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
 RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,
 RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
 RA Utechtback T.R., Cotton M.D., Spriggs T., Artlich P., Kaine B.P.,
 RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
 RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
 RA Moese C.R., Venter J.C.;
 RA Moese C.R., Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 DR EMBL; AE001045; AAB90383.1; -
 DR PIR; H69356; H69356.
 DR TIGR; AF0856;
 DR DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002825; DUF114.
 DR InterPro; IPR002142; Peptidase_S49.
 DR Pfam; PF01972; DUF114; 1.
 DR ProDom; PD002897; Peptidase_S49; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 291 AA; 32891 MW; 5D2C2978A80E628C CRC64;

Query Match 100.0%; Score 28; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
 Db 134 HYAMS 138

RESULT 19
 ID YB5_METUA STANDARD; PRT; 292 AA.
 AC YB5_METUA
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical protein MJ1495.
 GN OrderedlocusNames=MJ1495;

OS Methanococcus jannaschii.
 OC Archaea; Buryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 NCBI_TaxID=2190;
 RN NCBI_TaxID=2190;
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kierlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirschner E.F., Weinstock K.G., Furrick J.N., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utechtback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Huret M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.;
 RA Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- SIMILARITY: STRONG, TO M.JANNSCHII MJ0137.
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 CC -----
 DR EMBL; U67590; AAB99506.1; -
 DR PIR; F64486; F64486.
 DR TIGR; MJ1495; -
 DR InterPro; IPR002825; DUF114.
 DR Pfam; PF01972; DUF114; 1.
 KW Complete proteome; Hypothetical protein; Transmembrane.
 FT TRANSMEM 17 37 Potential.
 SQ SEQUENCE 292 AA; 33508 MW; BBA34C29B3A51246 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 292;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
 Db 135 HYAMS 139

RESULT 20
 ID Q8P8B3 PRELIMINARY; PRT; 292 AA.
 AC Q8P8B3;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DE Hypothetical protein XCC2330.
 DE Hypothetical protein XCC2330.
 GN OrderedlocusNames=XCC2330;
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 NCBI_TaxID=340;
 RN NCBI_TaxID=340;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Rainach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
 RA Camarotte G., Cannavan F., Cardoso J., Chamberg F., Ciapina L.P.,
 RA Ciccarelli R.M.B., Coutinho L.L., Curisno-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.,
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities."
 RL Nature 417:459-463(2002).
 RL EMBL; AE012341; AAM41608.1; -;
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 292 AA; 31426 MW; 24A2E2E9CEA2A858 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 292;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
 DB 70 HYAMS 74

RESULT 21

09Y9S6 PRELIMINARY; PRT; 295 AA.

AC 09Y9S6;
 DT 01-NOV-1999 (TEMBLrel. 12, Created)
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Hypothetical protein APE2212.

GN OrderedLocuNames=APB2212;
 OS Aeropyrum pernix.

OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
 OC Desulfurococcaceae; Aeropyrum.

NCBI_TaxID=56636;

SEQUENCE FROM N.A.

STRAIN=KI;

MEDLINE=99310339; PubMed=10382966;

RA Kwarabayaasi Y., Hino Y., Horikawa H., Yamazaki S., Hatake Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anki A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takahiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix KI.";

RT DNA Res. 6:83-101(1999).

EMBL; AP000063; BAA81224.1; -.

PIR; H72529; H72529.

InterPro; IPR002825; DUF114.

Pfam; PF01972; DUF114; 1.

KM Complete proteome; Hypothetical protein.

SQ SEQUENCE 295 AA; 32651 MW; 64D00C0E5C8D439 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
 DB 129 HYAMS 133

RESULT 22

08YQJ8 PRELIMINARY; PRT; 297 AA.

AC 08YQJ8;
 DT 01-MAR-2002 (TEMBLrel. 20, Created)
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE A13825 protein.

GN OrderedLocuNames=a13825;

OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostrocaceae; Nostoc.
 NCBI_TaxID=103690;

SEQUENCE FROM N.A.

MEDLINE=21595285; PubMed=11759840;

RA Kaneo T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iritani M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsumoto M., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.,
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120.";

RL DNA Res. 8:205-213(2001).

EMBL; AP003594; BAB75524.1; -.

PIR; AB2284; AB2284.

GO; GO:0008233; P:peptidase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002825; DUF114; 1.

InterPro; IPR002142; Peptidase_S49.

Pfam; PF01972; DUF114; 1.

ProDom; PD002897; Peptidase_S49; 1.

KM Complete proteome.

SQ SEQUENCE 297 AA; 33313 MW; 927BBF4D2EF29D1A CRC64;

Query Match 100.0%; Score 28; DB 2; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
 DB 122 HYAMS 126

RESULT 23

HEMZ_PORGI STANDARD; PRT; 345 AA.

Q7WXP4;

DT 29-MAR-2004 (Rel. 43, Created)

DT 23-MAR-2004 (Rel. 43, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Pterrochelatase (EC 4.99.1.1) (Prothème ferro-lyase) (Heme synthetase).

GN Name=heme; OrderedLocuNames=PG0127;

OS Porphyromonas gingivalis (Bacteroides gingivalis).

OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;

OC Porphyromonadaceae; Porphyromonas.

NCBI_TaxID=837;

SEQUENCE FROM N.A.

STRAIN=W83;

MEDLINE=22829867; PubMed=12949112;

RA Nelson K.E., Fleischmann R.D., Deboy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan W.J.,
 RA Dewhirst F.E., Fraser C.M.,
 RT "Complete genome sequence of the oral pathogenic bacterium
 RT Porphyromonas gingivalis strain W83.";

RT J. Bacteriol. 185:5591-5601(2003).

-1- FUNCTION: Catalyzes the ferrous insertion into protoporphyrin IX.

-1- CATALYTIC ACTIVITY: Protoporphyrin + Fe(2+) = protoheme + 2 H(+).

-1- PATHWAY: Protoheme biosynthesis; last step.

-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-1- SIMILARITY: Belongs to the ferrochelatase family.

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CC EMBL; AE017172; AA065369.1; -
DR TIGR; PG0127; -
DR HAMAP; MF_00323; -; 1.
DR InterPro; IPR001015; Retrochelatase.
DR Pfam; PF00762; Retrochelatase; 1.
DR ProDom; PD002792; Retrochelatase; 1.
DR TIGRFAMs; TIGR00109; hemH; 1.
DR PROSITE; PS00534; FERROCHELATASE; FALSE NEG.
KM Complete proteome; Heme biosynthesis; Iron; Lyase;
KW Porphyryn biosynthesis.
FT METAL 199 199 Iron (By similarity).
FT METAL 302 302 Iron (By similarity).
SQ SEQUENCE 345 AA; 39561 MW; 1A4D7EFB870012F CRC64;

Query Match 100.0%; Score 28; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 HYAMS 5
Db 137 HYAMS 141

RESULT 24
082871 PRELIMINARY; PRT; 424 AA.
AC 082871;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nhap.
GN Name=nhap;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=98322119; PubMed=9655928;
RA Uteng T., Inaba K., Kuroda T., Tsuda M., Tsuchiya T.;
RT "Cloning and sequencing of a novel Na+/H+ antiporter gene from
Pseudomonas aeruginosa."
RL Biochim. Biophys. Acta 1398:330-334(1998).
DR EMBL; AB010827; BA31695.1; -
DR PIR; C83159; C83159.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0015399; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006153; Na_Hporter.
DR Pfam; PF00999; Na_H_Exchange; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 424 AA; 45486 MW; 8E116A82C5825628 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 HYAMS 5
Db 272 HYAMS 276

RESULT 25
07DC93 PRELIMINARY; PRT; 424 AA.
AC 07DC93;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Na+/H+ antiporter Nhap.

GN Name=nhap; OrderedLocusNames=PA3887;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004806; AA007274.1; -
DR InterPro; IPR006153; Na_Hporter.
DR Pfam; PF00999; Na_H_Exchange; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 424 AA; 45486 MW; 8E116A82C5825628 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 HYAMS 5
Db 272 HYAMS 276

RESULT 26
08A516 PRELIMINARY; PRT; 448 AA.
AC 08A516;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative outer membrane protein TolC.
GN OrderedLocusNames=BT2253;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_Taxid=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VP1-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjureell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; AE016935; AA077360.1; -
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003423; OEP.
DR Pfam; PF02321; OEP; 2.
KW Complete proteome.
SQ SEQUENCE 448 AA; 51254 MW; E4DA4539991DFB28 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 HYAMS 5
Db 170 HYAMS 174

RESULT 27
06N245

ID Q6N245 PRELIMINARY; PRT; 453 AA.
AC Q6N245;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Possible polysaccharide export protein, PST family.
GN OrderedlocusNames=RPA4205;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Peres C.,
Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL: BX572606; CAE29646.1; -.
DR InterPro: IPR002797; PolySacc_synt.
DR Pfam: PF01943; PolySacc_synt; 1.
KW Complete proteome.
SQ SEQUENCE 453 AA; 48737 MW; 3FF259A02106193 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 296 HYAMS 300

RESULT 28
CAE29646 PRELIMINARY; PRT; 453 AA.
AC CAE29646;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Possible polysaccharide export protein, PST family.
GN RPA4205.
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J., Malfatti S., Do L.,
Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Peres C.,
Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL: BX572606; CAE29646.1; -.
SQ SEQUENCE 453 AA; 48737 MW; 3FF259A02106193 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 296 HYAMS 300

RESULT 29
Q89UC7 PRELIMINARY; PRT; 464 AA.
AC Q89UC7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE B11490 protein.
GN OrderedlocusNames=b11490;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamitsawa K., Uehiuni T.,
RA Sasamoto S., Matsumoto A., Idegawa K., Iriyuchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL: AP005940; BAC46755.1; -.
KW Complete proteome.
SQ SEQUENCE 464 AA; 50203 MW; 733DFC702255DD3E CRC64;

Query Match 100.0%; Score 28; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5
Db 309 HYAMS 313

RESULT 30
NUSM CANPA STANDARD; PRT; 555 AA.
AC P48919;
DT 01-FEB-1996 (Rel. 33, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 5 (BC 1.6.5.3) (NADH
dehydrogenase subunit 5).
GN Name=NDS; Synonyms=NAD5;
OS Candida parapsilosis (Yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5480;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SR23 / CBS 7157;
RX MEDLINE=94364940; PubMed=7521869;
RA Nosek J., Fukuhara H.;
RT "NADH dehydrogenase subunit genes in the mitochondrial DNA of
yeasts.";
RL J. Bacteriol. 176:5622-5630(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SR23 / CBS 7157;
RA Nosek J., Novotna M., Hlavatovicova Z., Ussery D.W., Fajkus J.,
RA Tomaska L.;
RT "Complete DNA sequence of the linear mitochondrial genome of the
pathogenic yeast Candida parapsilosis.";
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein, mitochondrial
inner membrane (Probable).
CC -1- SIMILARITY: Belongs to the complex I subunit 5 family.

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DR EMBL: X74411; CAES4609.1; -;
DR InterPro: IPR010934; NADH5 C.
DR InterPro: IPR003945; NADHPI_oxred5.
DR InterPro: IPR003916; NADHUB_oxred5.
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR001516; Oxidored_q1_N.
DR Pfam: PF06455; NADH5 C; 1.
DR Pfam: PF00361; Oxidored_q1; 1.
DR Pfam: PF00662; Oxidored_q1_N; 1.
DR PRINTS: PR01434; NADH5GNASES.
DR TIGRPFAM: TIGR01974; NDH_1_L; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 555 AA; 62517 MW; 60423C2CE556ACD CRC64;

Query Match 100.0%; Score 28; DB 1; Length 555;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 434 HYAMS 438

RESULT 31
COD2_YEAST STANDARD; PRT; 839 AA.

AC P53959;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE COD2 protein (complexed with DOR1 protein 2).
GN Name:COD2; Synonym:TR12; OrderedLocustNames=YVL041C; ORFNames=N2675;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D., Hilbert H.,
RA Moesli D.,
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SUBUNIT.
RX MEDLINE=21563418; PubMed=11703943;
RA Whyte J.R., Munro S.;
RT "The Sec34/35 Golgi transport complex is related to the exocyst,
RT defining a family of complexes involved in multiple steps of membrane
RT traffic";
RL Dev. Cell 11:527-537 (2001).
CC -1- SUBUNIT: Component of the Sec34/Sec35 complex which consists of
CC eight different proteins.
CC -1- SIMILARITY: Belongs to the COG6 family.

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DR EMBL: Z71317; CA95908.1; -;
DR FTR; S62963; S62963.
DR GenOnline; 143048; -;
DR SGD; S0004986; TFI2.

DR GO; GO:0017119; C:Golgi transport complex; IPT.
DR GO; GO:0006891; P:intra-Golgi transport; IGI.
DR InterPro: IPR010450; COG6.
DR Pfam: PF06419; COG6; 1.
KW Golgi stack; Membrane; Protein transport; Transport.
SQ SEQUENCE 839 AA; 96975 MW; 6484A40F99AD787 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 839;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 78 HYAMS 82

RESULT 32
Q6CHS4 PRELIMINARY; PRT; 1012 AA.

AC Q6CHS4;
DT 01-OCT-2004 (TEMBLrel. 28, Created)
DT 01-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Chromosome A of strain CU1B99 of Yarrowia lipolytica.
GN ORFNames=YALI0A05533g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CU1B99;
RG GENOEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neveglisse C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confantolero F., de Daruvar A.,
RA Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantaye F., Henneguin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Leaur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Ostas S., Ozer-Kalogreopoulos O.,
RA Pellenz S., Poelier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souclet J.L.;
RT "Genome evolution in yeasts";
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CU1B99;
RA Genoscope; (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR382127; CAG83712.1; -;
SQ SEQUENCE 1012 AA; 113158 MW; E12C7D1BF427807C CRC64;

Query Match 100.0%; Score 28; DB 2; Length 1012;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 36 HYAMS 40

RESULT 33
S24B_HUMAN STANDARD; PRT; 1268 AA.

AC Q95457;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Protein transport protein Sec24B (SEC24-related protein B).
 GN Name=SEC24B;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=99175155; PubMed=10075675;
 RA Pagano A., Letourneur F., Garcia-Estefania D., Carpenter J.-L.,
 RA Orci L., Paccard J.-P.;
 RT "Sec24 proteins and sorting at the endoplasmic reticulum";
 RL J. Biol. Chem. 274:7833-7840(1999).
 CC -1- FUNCTION: Component of the COP1 coat, that covers ER-derived
 vesicles involved in transport from the endoplasmic reticulum to
 the Golgi apparatus. COP1 acts in the cytoplasm to promote the
 transport of secretory, plasma membrane, and vacuolar proteins
 from the endoplasmic reticulum to the Golgi complex.
 CC -1- SUBUNIT: COP1 is composed of at least five proteins: the Sec23/24
 complex, the Sec13/31 complex and Sar1. Sec24B is capable of
 forming heterodimers with Sec24A.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and perinuclear.
 CC TISSUE SPECIFICITY: Expressed in fibroblasts, hepatocytes, and
 lymphocytes.
 CC -1- SIMILARITY: Belongs to the SEC23/SEC24 family. SEC24 subfamily.
 CC -----
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 CC -----
 DR EMBL: AJ131245; GCA10335.1; -.
 DR HSSP: P40482; 1M2V.
 DR Intact; O95487; -.
 DR Genew; HGNC:10704; SEC24B.
 DR MIM; 607184; -.
 DR GO; GO:0030138; C:COPII-coated vesicle; TAS.
 DR GO; GO:0016020; C:membrane; TAS.
 DR GO; GO:0005215; F:Transporter activity; TAS.
 DR GO; GO:0016192; P:Vesicle-mediated transport; TAS.
 DR InterPro; IPR001123; Gelsolin.
 DR InterPro; IPR006900; Sec23_helical.
 DR InterPro; IPR006896; Sec23_trunk.
 DR InterPro; IPR006895; zf-Sec23_Sec24.
 DR Pfam; PF00626; Gelsolin; 1.
 DR Pfam; PF04815; Sec23_helical; 1.
 DR Pfam; PF04811; Sec23_trunk; 1.
 DR Pfam; PF04810; zf-Sec23_Sec24; 1.
 KM Endoplasmic reticulum; Golgi stack; Multigene family;
 KW Protein transport; Transport.
 FT DOMAIN 605 629 Zinc finger-like.
 FT DOMAIN 379 387 Poly-Glu.
 SQ SEQUENCE 1268 AA; 137788 MW; 7FCA4907CBB32FF9 CRC64;
 QY 1 HYAMS 5
 Db 182 HYAMS 186
 Query Match 100.0%; Score 28; DB 1; Length 1268;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG31756-PA.
 GN ORFNames=CG31756;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabo G.L.,
 RA Abril J.F., Abpayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostel C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glorok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin M., Houston K.A., Howland T.J., Wei M.H., Ibbegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazolo W., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirekas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J., Ye J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Ceiniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacle J.W., Park S., Pfeiffer B.D., Richards S., Sodegren E.J.,
 RA Swirekas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers S.E., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Swirekas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Ceiniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Ceolnik S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.D., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN
 RP SEQUENCE FROM N.A.
 RG FLVBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FLVBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003620; AAF52603.3; -.
 DR Inact; O9VLT1; -.
 DR FLVBASE; FBgn0031985; CG8683.
 DR INTERPRO; IPR008938; ARM.
 SQ SEQUENCE 1675 AA; 185904 MW; EA5A3DD1943FF96E CRC64;
 Query Match 100.0%; Score 28; DB 2; Length 1675;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYAMS 5
 DB 572 HYAMS 576
 RESULT 35
 ID Q86DB6 PRELIMINARY; PRT; 19 AA.
 AC Q86DB6;
 DT 01-JUN-2003 (TREMblrel. 24, Created)
 DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Homobox protein Otx (Fragment).
 GN Name=Hroch;
 OS Halocynthia roretzi (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyuridae; Halocynthia.
 OC NCBI_TaxID=7729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22586101; PubMed=12701103;
 RA Oda-Ishii I., Saiga H.;
 RT "Genomic organization and promoter and transcription regulatory
 RT regions for the expression in the anterior brain (sensory vesicle) of
 RT Hroch, the otx homologue of the ascidian, Halocynthia roretzi.";
 RL Dev. Dyn. 227:104-113(2003).
 DR EMBL; AB104851; BAC76068.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 KW Nuclear protein.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2041 MW; 2D9CAB7036EAF8D CRC64;
 Query Match 89.3%; Score 25; DB 2; Length 19;
 Best Local Similarity 80.0%; Pred. No. 69;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYAMS 5
 DB 8 HYAMN 12
 RESULT 36
 ID Q6TFAB PRELIMINARY; PRT; 56 AA.
 AC Q6TFAB;

DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Aeromonas hydrophila.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; Aeromonas.
 OC NCBI_TaxID=644;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PPD134/91;
 RX MEDLINE=20244644; PubMed=10784058;
 RA Zhang Y.L., Ong C.T., Leung K.Y.;
 RT "Molecular analysis of genetic differences between virulent and
 RT avirulent strains of Aeromonas hydrophila isolated from diseased
 RT fish.";
 RL Microbiology 146:999-1009(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PPD134/91;
 RA Lau Y.L., Leung K.Y.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY422732; AAR06612.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 56 AA; 6246 MW; 13F2CF2A13635440 CRC64;
 Query Match 89.3%; Score 25; DB 2; Length 56;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYAMS 5
 DB 23 HYALS 27

RESULT 37
 ID AAR06612 PRELIMINARY; PRT; 56 AA.
 AC AAR06612;
 DT 02-MAR-2004 (TREMblrel. 27, Created)
 DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Aeromonas hydrophila.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; Aeromonas.
 OC NCBI_TaxID=644;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PPD134/91;
 RX MEDLINE=20244644; PubMed=10784058;
 RA Zhang Y.L., Ong C.T., Leung K.Y.;
 RT "Molecular analysis of genetic differences between virulent and
 RT avirulent strains of Aeromonas hydrophila isolated from diseased
 RT fish.";
 RL Microbiology 146:999-1009(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PPD134/91;
 RA Lau Y.L., Leung K.Y.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY422732; AAR06612.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 56 AA; 6246 MW; 13F2CF2A13635440 CRC64;
 Query Match 89.3%; Score 25; DB 2; Length 56;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYAMS 5
 DB 23 HYALS 27

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RESULT 38
Q8GWL8      PRELIMINARY;      PRT;      60 AA.
ID Q8GWL8;
AC Q8GWL8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein At5g47830/MCA23_17.
GN Name=At5g47830/MCA23_17;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK118767; BAC43360.1; -.
KW Hypothetical protein.
SQ SEQUENCE 60 AA; 6671 MW; 6DAECA745A15FEF7 CRC64;

Query Match      89.3%; Score 25; DB 2; Length 60;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 2 HYAMN 6

RESULT 39
Q8HM19      PRELIMINARY;      PRT;      98 AA.
ID Q8HM19;
AC Q8HM19;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 4L.
GN Name=ND4L;
OS Caulophryne pelagica.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Lophiiformes; Ceratioidei;
OC Ceratioidei; Caulophrynidae; Caulophryne.
OX NCBI_TaxID=181422;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2359432; Pubmed=12470944;
RA Miya M., Takeshima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T.,
RA Satoh T.P., Yamaguchi M., Kawaguchi A., Nabuchi K., Shirai S.M.,
RA Nishida M.;
RT "Major patterns of higher teleostean phylogenies: a new perspective
RT based on 100 complete mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 26:121-138(2003).
DR EMBL; AP004417; BAC23341.1; -.
GO GO; GO:0005739; C:mitochondrion; IEA.
GO GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR001133; Oxidored 4L.
DR InterPro; IPR003214; Oxidored4L.
DR Pfam; PF00420; Oxidored_g2; 1.
DR Prodom; PD000359; Oxidred4L; 1.
KW Mitochondrion.
SQ SEQUENCE 98 AA; 10424 MW; 420933289F1ECDC1 CRC64;

Query Match      89.3%; Score 25; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HYAMS 5
Db 5 HYALS 9

RESULT 40
Q8RBB0      PRELIMINARY;      PRT;      116 AA.
ID Q8RBB0;
AC Q8RBB0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=TR0912;
OS Thermoaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoaerobacteriales;
OC Thermoaerobacteriaceae; Thermoaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=21992816; Pubmed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013057; AAM24168.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 116 AA; 12794 MW; 61E3EB46A6B2F1 CRC64;

Query Match      89.3%; Score 25; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db 36 HYSMS 40

Search completed: December 17, 2004, 19:14:36
Job time : 16.9438 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:10:02 ; Search time 51.6665 Seconds
(without alignments)
118.029 Million cell updates/sec

Title: US-10-089-500-4

Perfect score: 89

Sequence: 1 YISGSGSGTRYSDSVK 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_23Sep04:*
2: geneseqp1980s:*
3: geneseqp1980s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	89	100.0	17 4 AAB81980	Aab81980 Gangliosid
2	89	100.0	17 6 ABU11005	Abu11005 Modified
3	89	100.0	119 4 AAB81985	Aab81985 Gangliosid
4	89	100.0	119 4 AAB81989	Aab81989 Gangliosid
5	89	100.0	119 6 ABU11012	Abu11012 Modified
6	89	100.0	119 6 ABU11010	Abu11010 Modified
7	89	100.0	130 2 AAR33256	Aar33256 Rat Immun
8	89	100.0	130 2 AAR53341	Aar53341 Km641 L c
9	89	100.0	130 2 AAY28369	Aay28369 PKM641 RA
10	89	100.0	130 3 AAB01627	Aab01627 Murine im
11	89	100.0	138 4 AAB81977	Aab81977 Gangliosid
12	89	100.0	138 6 ABU11002	Abu11002 Modified
13	89	100.0	582 4 AAB81987	Aab81987 Gangliosid
14	89	100.0	582 4 AAB81991	Aab81991 Gangliosid
15	89	100.0	119 2 AAW11919	Aaw11919 Humanised
16	89	100.0	247 2 AAW11917	Aaw11917 Murine MA
17	89	100.0	118 2 AAR41233	Aar41233 Monoclonal
18	89	100.0	17 7 ADJ95630	Adj95630 Rat Insul
19	89	100.0	118 7 ADJ95639	Adj95639 Insulin-1
20	89	100.0	137 7 ADJ95626	Adj95626 Rat Insul
21	89	100.0	117 8 ADG25805	Adg25805 Ant1-CD30
22	89	100.0	120 7 ADC27437	Adc27437 TMEFF2#10
23	89	100.0	237 5 ABP46028	Abp46028 Human Bly
24	89	100.0	237 5 ABP45895	Abp45895 Human Bly
25	89	100.0	237 7 ADG96722	Adg96722 Single ch

26	72	80.9	237	7	ADG96855	Adg96855 Single ch
27	72	80.9	240	5	ABP45894	Abp45894 Human Bly
28	72	80.9	240	7	ADG96721	Adg96721 Single ch
29	72	80.9	246	7	ADG30412	Adg30412 Human GMB
30	72	79.8	136	2	AAR06251	Aar06251 Variable
31	71	79.8	247	1	AAP80156	Aap80156 Biosynthe
32	71	79.8	249	4	AAB20436	Aab20436 Anti-FIX
33	71	79.8	249	4	AAB20435	Aab20435 Anti-FIX
34	71	79.8	294	4	AAB20442	Aab20442 Anti-FIX
35	71	79.8	325	4	AAB20438	Aab20438 Anti-FIX
36	71	79.8	732	4	AAB20437	Aab20437 Anti-FIX
37	70	78.7	119	2	AAR82986	Aar82986 LK26 huma
38	70	78.7	119	2	AAR82980	Aar82980 LK26 huma
39	70	78.7	119	2	AAR82981	Aar82981 LK26 huma
40	70	78.7	119	2	AAR82982	Aar82982 LK26 huma
41	70	78.7	119	2	AAR82979	Aar82979 LK26 huma
42	70	78.7	119	2	AAR82977	Aar82977 LK26 heav
43	70	78.7	121	3	AAY96063	Aay96063 Human ant
44	69	77.5	21	2	AAW95565	Aaw95565 Immunoglo
45	69	77.5	30	2	AAW95570	Aaw95570 Immunoglo

ALIGNMENTS

RESULT 1
AAB81980
ID AAB81980 standard; peptide, 17 AA.

AC AAB81980;
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related peptide SEQ ID NO: 4.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW Cancer.

OS Mus musculus.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP06774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

(KYOW) KYOWA HAKKO KOGYO KK.
Hanai N, Shitara K, Nakamura K, Niwa R;

WPI, 2001-266143/27.

PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.

PS Claim 5; Page 141; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumours, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention

SO Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4; 1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YISSGSGGTYSDSVKG 17
 |||||
 DB 1 YISSGSGGTYSDSVKG 17

RESULT 2

ABU1005
 ID ABU1005 standard; peptide; 17 AA.

AC AAB1005;
 XX

DT 04-FEB-2003 (first entry)
 XX

DE Modified ganglioside GD3 antibody associated peptide #2.
 XX

KM Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 XX

OS Mus musculus.
 XX

PN W0200278739-A1.
 XX

PD 10-OCT-2002.
 XX

PF 29-MAR-2002; 2002WO-JP003170.
 XX

PR 29-MAR-2001; 2001JP-00097483.
 XX

PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX

PI Shitara K, Niwa R, Kanazawa J, Asada M;
 XX

DR WPI; 2003-067410/06.
 XX

PT Drug containing genetically-modified antibody against ganglioside GD3,
 its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX

PS Claim 6; Page 98; 121pp; Japanese.
 XX

CC The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a peptide associated with the anti- ganglioside GD3 antibody
 CC
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.1e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YISSGSGGTYSDSVKG 17
 |||||
 DB 1 YISSGSGGTYSDSVKG 17

RESULT 3

AAB81985
 ID AAB81985 standard; protein; 119 AA.

AC AAB81985;
 XX

DT 03-JUL-2001 (first entry)
 XX

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.
 XX

KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
 cancer.
 XX

OS Synthetic.

PN W0200123432-A1.
 XX

PD 05-APR-2001.
 XX

PF 29-SEP-2000; 2000WO-JP006774.
 XX

PR 30-SEP-1999; 99JP-00278291.
 XX

PR 06-APR-2000; 2000JP-00105088.
 XX

PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX

PI Hanai N, Shitara K, Nakamura K, Niwa R;
 XX

DR WPI; 2001-266143/27.
 XX

PT New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumours, with low antigenicity, little side effects but potent
 PT activity in cancer.
 XX

PS Claim 20; Page 142-143; 183pp; Japanese.
 XX

CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumours, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 XX

SQ Sequence 119 AA;

Query Match 100.0%; Score 89; DB 4; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YISSGSGGTYSDSVKG 17
 |||||
 DB 50 YISSGSGGTYSDSVKG 66

RESULT 4

AAB81989
 ID AAB81989 standard; protein; 119 AA.

AC AAB81989;
 XX

DT 03-JUL-2001 (first entry)
 XX

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.
 XX

KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
 cancer.
 XX

OS Mus musculus.
 XX

PN W0200123432-A1.
 XX

PD 05-APR-2001.
 XX

PF 29-SEP-2000; 2000WO-JP006774.
 XX

PR 30-SEP-1999; 99JP-00278291.
 XX

PR 06-APR-2000; 2000JP-00105088.
 XX

PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX

PI Hanai N, Shitara K, Nakamura K, Niwa R;
 XX

DR WPI; 2001-266143/27.
 XX

PT New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.

PS Claim 10; Page 173-174; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 89; DB 4; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISGGSGGTYSDSVKG 17
|||||
DB 50 YISGGSGGTYSDSVKG 66

RESULT 5

ABU11012
ID ABU11012 standard; protein; 119 AA.

XX ABU11012;

XX 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #5.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Mus musculus.

XX WO200278739-A1.

XX 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

PT Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and anticancer agents in
PT combination, applicable in treating malignant tumor like melanoma.

PS Claim 7; Page 112-113; 121pp; Japanese.

CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 89; DB 6; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISGGSGGTYSDSVKG 17
|||||

DB 50 YISGGSGGTYSDSVKG 66

RESULT 6

ABU11010
ID ABU11010 standard; protein; 119 AA.

XX ABU11010;

XX 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #3.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Synthetic.

XX WO200278739-A1.

XX 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

PT Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and anticancer agents in
PT combination, applicable in treating malignant tumor like melanoma.

XX Claim 8; Page 99; 121pp; Japanese.

CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 89; DB 6; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISGGSGGTYSDSVKG 17
|||||
DB 50 YISGGSGGTYSDSVKG 66

RESULT 7

AAR33256
ID AAR33256 standard; protein; 130 AA.

XX AAR33256;

XX 25-MAR-2003 (revised)

DT 12-UTL-1993 (first entry)

DE Rat immunoglobulin H chain variable region of pKX641HA3.

XX Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
KW humanised; chimeric; antibody; expression vector.

XX Rattus rattus.
XX

FH	Key	location/Qualifiers
FT	Peptide	1..10 "Signal peptide"
FT	Protein	11..130
FT		/note= "Mature protein"
XX		
PN	EP533199-A2.	
XX		
PD	24-MAR-1993.	
XX		
PF	18-SEP-1992;	92EP-00116026.
XX		
PR	18-SEP-1991;	91JP-00238375.
XX		
PA	(KYOW) KYOWA HAKKO KOGYO CO LTD.	
XX		
PI	Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y,	
XX		
DR	WPI, 1993-095510/12.	
XX	N-PSDB; AAQ33257.	
XX		
PT	Humanised chimeric antibody prodn. against ganglioside GD3 - for treating	
XX	cancers, such as melanoma, neuroblastoma, etc.	
XX		
ES	Claim 6; Page 29-30; 63pp; English.	
XX		
CC	The sequences given in AAR33256-57 represent rat heavy and light chain	
CC	variable regions respectively. The DNA sequences encoding these proteins	
CC	were used in the construction of humanised chimeric antibody expression	
CC	vectors. In these humanised antibodies none of the amino acids of the non	
CC	-human animal Ab variable region have been changed. (Updated on 25-MAR-	
CC	2003 to correct FN field.)	
XX		
SQ	Sequence 130 AA;	
	Query Match	100.0%; Score 89; DB 2; Length 130;
	Best Local Similarity	100.0%; Pred. No. 3.6e-05;
	Matches 17; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
OY	1 YISSGSGSTYYSDSVKG 17	
DB	60 YISSGSGSTYYSDSVKG 76	
	RESULT 8	
	AAR53341	
ID	AAR53341 standard; protein; 130 AA.	
XX		
AC	AAR53341;	
XX		
DT	18-NOV-1994 (first entry)	
XX		
DE	KM641 L chain variable region.	
XX		
KW	Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;	
KW	expression vector; heavy; light; chain; hypervariable region; CDR;	
KW	constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.	
OS	Mus musculus.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..10
FT		/label= sig_peptide
XX		
PN	AU9346181-A.	
XX		
PD	17-MAR-1994.	
XX		
PF	07-SEP-1993;	93AU-00046181.
XX		
PR	07-SEP-1992;	92JP-00238452.
XX		
PA	(KYOW) KYOWA HAKKO KOGYO KK.	

XX	Nakamura K,	Koike M,	Shitara K,	Hanai N,	Kuwana Y,	Haasegawa M;
PI						
DR	WPI; 1994-126857/16.					
DR	N-PSDB; AAQ45439.					
XX						
PT	Humanised antibody specific for ganglioside GM2 - used for producing a					
PT	cytocidal effect on cancers such as melanoma, neuroblastoma and glioma.					
XX						
PS	Example 2; Page 116-117; 191pp; English.					
XX						
CC	Example 2 describes the construction of the vector pChl641HA1 for					
CC	chimeric human antibody H chain expression. mRNA from mouse anti-GD3					
CC	monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain					
CC	CDNA's isolated. The base sequences of the Ig variable regions in KM641 H					
CC	chain CDNA (PKM641HA3) and KM641 L chain cDNA (PKM641LA2) are given in					
CC	AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector					
CC	was constructed by joining the H chain variable region gene from					
CC	PKM641HA3 to a vector for chimeric human Ab H chain expression using the					
CC	synthetic DNAs given in AAQ63439 and AAQ63440					
XX						
SQ	Sequence 130 AA;					
Query Match		100.0%;	Score 89;	DB 2;	Length 130;	
Best Local Similarity		100.0%;	Pred. No. 3.6e-05;			
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
OY	1 YISSGSGGTYYSDSVKG 17 60 YISSGSGGTYYSDSVKG 76					
Db						
RESULT 9						
AAZ28369						
ID	AAZ28369 standard; protein; 130 AA.					
AC	AAZ28369;					
XX						
DT	04-NOV-1999 (first entry)					
XX						
DE	pKM641 HA3 immunoglobulin heavy chain.					
XX						
KM	antibody; nucleotide; genomic; hypervariable region; chimeric;					
KW	light chain; amino acid.					
XX						
OS	Mus sp.					
XX						
PN	US5939532-A.					
XX						
PD	17-AUG-1999.					
XX						
PF	07-JUN-1995; 95US-00483528.					
XX						
PR	07-SEP-1993; 93US-00116778.					
XX						
PA	(KYOW) KYOMA HAKKO KOGYO KK.					
XX						
PI	Nakamura K, Hanai N, Kuwana Y, Haasegawa M, Koike M, Shitara K;					
XX						
DR	WPI; 1999-468416/39.					
DR	N-PSDB; AAX99482.					
XX						
PT	Chimeric human antibody expression vectors.					
XX						
PS	Example 1; Col 99-101; 188pp; English.					
XX						
CC	This immunoglobulin region was isolated from PKM641HA3. This sequence has					
CC	no methionine initiation codon and the leader sequence was partly					
CC	lacking. The chimeric human antibodies are useful in the treatment of					
CC	cancer, especially that which is of neural ectodermal origin. In contrast					
CC	to prior art constructs based on mouse monoclonal antibodies, the					
CC	chimeric human antibodies do not cause anti-mouse immunoglobulin					
CC	production. The chimeric human antibodies have a prolonged half-life and					

CC a reduced frequency of adverse effects when compared to mouse monoclonal
 CC antibodies
 XX
 SO Sequence 130 AA;

Query Match 100.0%; Score 89; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YISSGSGSTGYSDSVKG 17
 |||||
 DB 60 YISSGSGSTGYSDSVKG 76

RESULT 10
 AAB01627
 ID AAB01627 standard; protein; 130 AA.

AC AAB01627;
 XX
 DT 07-DEC-2000 (first entry)

DE Murine immunoglobulin heavy chain variable region.

KM Mouse; immunoglobulin; H chain; heavy chain; variable region; cancer;
 KM humanised antibody.

OS Mus sp;

PH Key Location/Qualifiers
 FT Peptide 1..10
 FT Protein /label= signal_peptide 11..130

FT /label= mature_immunoglobulin_heavy_chain_variable region

XX EP1013761-A2.

XX 28-JUN-2000.

XX 18-SEP-1992; 99EP-00124345.

XX 18-SEP-1991; 91JP-00238375.

XX 18-SEP-1992; 92EP-00116026.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;

XX WPI; 2000-402204/35.

XX N-PSDB; AAA51003.

PT New humanised chimera antibody KM-871 useful for treating cancer.
 PT comprises variable region of mouse monoclonal antibody, reactive with
 PT ganglioside and human antibody constant region.

PS Claim 14; Page 27-28; 65pp; English.

XX The present sequence is a murine immunoglobulin heavy chain variable
 CC region from plasmid KM-641. The coding sequence was used in the creation
 CC of an expression vector, along with the sequence for a human antibody, to
 CC produce humanised chimaeric antibodies, which can be used to treat
 CC cancer. Humanised chimaeric antibodies are more effective than mouse
 CC antibodies as they do not provoke a reaction in the human and side
 CC effects, such as the formation of anti-mouse immunoglobulin antibody and
 CC the rapid half-life of the immunoglobulins, do not occur

XX Sequence 130 AA;

Query Match 100.0%; Score 89; DB 3; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YISSGSGSTGYSDSVKG 17

DB |||||
 60 YISSGSGSTGYSDSVKG 76

RESULT 11
 AAB81977
 ID AAB81977 standard; protein; 138 AA.

XX AAB81977;

XX 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.

KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
 KM cancer.

OS Mus musculus.

XX WO200123432-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

XX 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.

XX

PT New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3. The antibody and its derivatives are
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.

XX

PS Example 1; Page 138-139; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention

XX

XX Sequence 138 AA;

Query Match 100.0%; Score 89; DB 4; Length 138;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YISSGSGSTGYSDSVKG 17
 |||||
 DB 69 YISSGSGSTGYSDSVKG 85

RESULT 12
 ABU11002
 ID ABU11002 standard; protein; 138 AA.

XX ABU11002;

XX 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #1.

KM Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Mus musculus.

XX WO200278739-A1.

XX 10-OCT-2002.
PD
XX
XX 29-MAR-2002; 2002WO-JP003170.
PF
XX 29-MAR-2001; 2001JP-00097483.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Shitara K, Niwa R, Kanazawa J, Asada M;
PI WPI; 2003-067410/06.
DR
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
PS Example 3; Page 97; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ Sequence 138 AA;
XX
Query Match 100.0%; Score 89; DB 6; Length 138;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YISSGSGGTYSDSVKG 17
Db 69 YISSGSGGTYSDSVKG 85
XX
RESULT 13
AAB81987
ID AAB81987 standard; protein; 582 AA.
XX
AC AAB81987;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW Cancer.
XX
XX Synthetic.
OS
XX WO200123432-A1.
PN
XX
XX 05-APR-2001.
PD
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI WPI; 2001-266143/27.
DR
XX
XX New human type complementation-determining region-transplanted antibody
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.

XX Claim 41; Page 168-172; 183pp; Japanese.
PS
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;
XX
Query Match 100.0%; Score 89; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YISSGSGGTYSDSVKG 17
Db 50 YISSGSGGTYSDSVKG 66
XX
RESULT 14
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW Cancer.
XX
XX Synthetic.
OS
XX WO200123432-A1.
PN
XX 05-APR-2001.
PD
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI WPI; 2001-266143/27.
DR
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Claim 39; Page 175-179; 183pp; Japanese.
PS
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;
XX
Query Match 100.0%; Score 89; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YISSGSGGTYSDSVKG 17
Db 50 YISSGSGGTYSDSVKG 66

RESULT 15
AAW11919
ID AAW11919 standard; protein; 119 AA.
XX
AC AAW11919;
XX
DT 16-OCT-2003 (revised)
DT 24-JUN-1997 (first entry)
XX
DE Humanised MAb SK48-E26 heavy chain.
XX
KW Interleukin-1 beta; IL-1 beta; recombinant antibody; humanised antibody;
KW chimeric antibody; antibody engineering; monoclonal antibody; MAb;
KW SK48-E26; inflammation; therapy.
XX
OS Homo; sapiens.
OS Mus sp.
OS Chimeric.
XX
FT Key Location/Qualifiers
FT 1..30
FT /label= FR1
FT /note= "framework region 1"
FT 31..35
FT /label= CDR1
FT /note= "complementarity determining region 1 (Claim 10,
FT page 48)"
FT 36..49
FT /label= FR2
FT /note= "framework region 2"
FT 50..66
FT /label= CDR2
FT /note= "complementarity determining region 2 (Claim 10,
FT page 48)"
FT 67..98
FT /label= FR3
FT /note= "framework region 3"
FT 99..108
FT /label= CDR3
FT /note= "complementarity determining region 3 (Claim 10,
FT page 48)"
FT 109..119
FT /label= FR4
FT /note= "framework region 4"
XX
PN WO9501997-A1.
XX
PD 19-JAN-1995.
XX
XX
PF 07-JUL-1994; 94WO-US007659.
XX
PR 09-JUL-1993; 93US-00090534.
PR 04-MAR-1994; 94US-00206190.
XX
PA (SMK) SMITHKLINE BEECHAM CORP.
XX
PI Young PR, Groves MS, Jonak ZL, Theisen TW, Hurle MR, Jackson JR;
XX WPI; 1995-066868/09.
XX DR N-PSDB; AAT51438.
XX
XX
PT Recombinant and humanised chimeric antibodies against human interleukin-1
PT -beta - for preventing and treating interleukin-mediated inflammatory
PT disorders.
XX
XX
PS Claim 39; Page 40-41; 62pp; English.
XX
XX
CC The heavy chain variable region (AAW11919) and light chain variable
CC region (AAW11920) of humanised anti-human interleukin-1 beta (IL-1 beta)
CC murine monoclonal antibody (MAb) SK48-E26 comprise the complementarity
CC determining regions from MAb SK48-E26 (see also AAW11917-18) grafted into
CC human frameworks. The humanised antibody can be produced in e.g. COS

CC cells transfected with vectors carrying humanised heavy and light chain
CC nucleic acids (AAT51437-39) for use in the treatment and prevention of IL
CC -1 mediated inflammatory disorders. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 119 AA;
XX
Query Match 86.5%; Score 77; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.0019;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 YISGSGGTYSDSVKG 17
||| ||| ||| ||| |||
Db 50 YISGSGGTYPDVKG 66
XX
RESULT 16
AAW11917
ID AAW11917 standard; protein; 247 AA.
XX
AC AAW11917;
XX
DT 24-JUN-1997 (first entry)
XX
DE Murine MAb SK48-E26 heavy chain.
XX
KW Interleukin-1 beta; IL-1 beta; recombinant antibody; humanised antibody;
KW chimeric antibody; antibody engineering; monoclonal antibody; MAb;
KW SK48-E26; inflammation; therapy.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FH 1..19
FH /label= Sig_peptide
FT 20..49
FT /label= FR1
FT /note= "framework region 1"
FT 50..54
FT /label= CDR1
FT /note= "complementarity determining region 1 (Claim 10,
FT page 48)"
FT 55..68
FT /label= FR2
FT /note= "framework region 2"
FT 69..85
FT /label= CDR2
FT /note= "complementarity determining region 2 (Claim 10,
FT page 48)"
FT 86..117
FT /label= FR3
FT /note= "framework region 3"
FT 118..127
FT /label= CDR3
FT /note= "complementarity determining region 3 (Claim 10,
FT page 48)"
FT 128..138
FT /label= FR4
FT /note= "framework region 4"
FT 139..247
FT /label= Constant_region
XX
XX
PN WO9501997-A1.
XX
PD 19-JAN-1995.
XX
XX
PF 07-JUL-1994; 94WO-US007659.
XX
PR 09-JUL-1993; 93US-00090534.
PR 04-MAR-1994; 94US-00206190.
XX
PA (SMK) SMITHKLINE BEECHAM CORP.
XX

PI Young PR, Gross MS, Jonak ZL, Theisen TW, Hurle MR, Jackson JR;
XX WPI; 1995-066868/09.
DR N-PSDB; AAT51436.
XX
XX
PT Recombinant and humanised chimeric antibodies against human interleukin-1
PT beta - for preventing and creating interleukin-mediated inflammatory
PT disorders.
XX
XX
PS Claim 5; Page 36-37; 62pp; English.
XX
XX
CC Amino acid sequences of the heavy chain (AAW11917) and light chain
CC (AAW11918) of anti-human interleukin-1 beta (IL-1 beta) murine monoclonal
CC antibody (Mab) SK48-E26 were deduced from nucleic acids (AAT51436-37)
CC derived from hybridoma SK48-E26. The heavy and light chains, esp. the
CC complementarity determining region sequences, can be utilised in novel
CC recombinant chimeric and humanised antibodies (see also AAW11919-20)
CC useful for the treatment and prevention of IL-1 mediated inflammatory
CC disorders
XX
SQ Sequence 247 AA;

Query Match 86.5%; Score 77; DB 2; Length 247;
Best Local Similarity 82.4%; Pred. No. 0.0041; 2; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGGSGTGYSDSVKG 17
Db 69 YISSGGSGTGYPTVKG 85

RESULT 17
AAR41233
ID AAR41233 standard; protein; 118 AA.
XX
AC AAR41233;
XX
DT 25-MAR-2003 (revised)
DT 18-MAR-1994 (first entry)
XX
DE Monoclonal antibody BW2121 V-gene heavy chain region.
XX
KM Monoclonal antibody; tumour; melanoma.
XX
OS Mus musculus.
XX
PN EP561183-A1.
XX
PD 22-SEP-1993.
XX
PF 25-FEB-1993; 93EP-00102895.
XX
PR 19-MAR-1992; 92DE-04208795.
XX
PA (BEHW) BEHRINGWERKE AG.
XX
PI Bosslet K, Seemann G, Dippold W;
XX
DR WPI; 1993-296513/38.
DR N-PSDB; AAO48765.
XX
XX
PT Hybridoma 2121 (dem acc 2036) and monoclonal antibody BW 2121 -
PT specifically bind to gangliosides GD3 and GQ1b, useful for prodn. and
PT diagnosis of melanoma or tumours expressing GD3 and GQ1b.
XX
PS Claim 2; Page 5; 9pp; German.
XX
XX
CC The monoclonal antibody BW2121 can be used for the detection of melanomas
CC and other tumours expressing GD3 and GQ1b. The monoclonal antibody may
CC also be used as part of a pharmaceutical composition or diagnostic kit.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 118 AA;

Query Match 84.3%; Score 75; DB 2; Length 118;
Best Local Similarity 82.4%; Pred. No. 0.0036; 2; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGGSGTGYSDSVKG 17
Db 50 YISSGGASTYRDSVKG 66

RESULT 18
ADJ95630
ID ADJ95630 standard; peptide; 17 AA.
XX
AC ADJ95630;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat insulin-like growth factor (IGF)-related peptide #2.
XX
XX
KM Insulin-like growth factor; IGF-I; IGF-II; diabetes;
KM rheumatoid arthritis; cancer; rat.
XX
OS Rattus norvegicus.
XX
PN WO2003093317-A1.
XX
PD 13-NOV-2003.
XX
PP 30-APR-2003; 2003WO-JP005505.
XX
PR 30-APR-2002; 2002JP-00129046.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Shitara K, Nakamura K, Furuya A, Niwa R, Ohki Y, Hanai N;
XX
DR WPI; 2003-854482/79.
XX
PT Antibodies and antibody fragments recognising human insulin-like growth
PT factor for treatment and diagnosis of cancer, diabetes and rheumatoid
PT arthritis.
XX
XX
PS Claim 3; SEQ ID NO 6; 115pp; Japanese.
XX
CC The invention comprises antibodies and antibody fragments which bind to
CC and inhibit the function of human insulin-like growth factor (IGF-I
CC and/or IGF-II). The antibodies and antibody fragments of the invention
CC are useful for the treatment, prevention, and diagnosis of diabetes,
CC rheumatoid arthritis and cancer. The present amino acid sequence
CC represents a rat insulin-like growth factor-related peptide of the
CC invention.
XX
SQ Sequence 17 AA;

Query Match 83.1%; Score 74; DB 7; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.0063; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTGYSDSVKG 17
Db 1 YISSGGSGTGYRDSVKG 17

RESULT 19
ADJ95639
ID ADJ95639 standard; protein; 118 AA.
XX
AC ADJ95639;
XX
DT 06-MAY-2004 (first entry)
XX
DE Insulin-like growth factor (IGF)-related protein #1.

XX insulin-like growth factor; IGF-I; IGF-II; diabetes;
KW rheumatoid arthritis; cancer.
XX
XX Unidentified.
OS
XX WO2003093317-A1.
PN
XX
XX 13-NOV-2003.
PD
XX 30-APR-2003; 2003WO-JP005505.
PF
XX 30-APR-2002; 2002JP-00129046.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX
XX Shitara K, Nakamura K, Furuya A, Niwa R, Ohki Y, Hanai N;
PI
XX WPI; 2003-854482/79.
DR
XX
XX Antibodies and antibody fragments recognizing human insulin-like growth
PT factor for treatment and diagnosis of cancer, diabetes and rheumatoid
PT arthritis.
XX
XX Example 7; SEQ ID NO 15; 115bp; Japanese.
PS
XX
XX The invention comprises antibodies and antibody fragments which bind to
CC and inhibit the function of human insulin-like growth factor (IGF-I
CC and/or IGF-II). The antibodies and antibody fragments of the invention
CC are useful for the treatment, prevention, and diagnosis of diabetes,
CC rheumatoid arthritis and cancer. The present amino acid sequence
CC represents an insulin-like growth factor-related protein of the
CC invention.
XX
XX
SQ Sequence 118 AA;

Query Match 83.1%; Score 74; DB 7; Length 118;
Best Local Similarity 82.4%; Pred. No. 0.005;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGCTYYSDSVKG 17
DB 50 YISSGGSGCTYYRDSVKG 66

RESULT 20
ADJ95626
ID ADJ95626 standard; protein; 137 AA.
XX
XX ADJ95626;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Rat insulin-like growth factor (IGF)-related protein #1.
DE
XX
XX Insulin-like growth factor; IGF-I; IGF-II; diabetes;
KW rheumatoid arthritis; cancer; rat.
XX
XX Rattus norvegicus.
OS
XX
XX WO2003093317-A1.
PN
XX
XX 13-NOV-2003.
PD
XX
XX 30-APR-2003; 2003WO-JP005505.
PF
XX
XX 30-APR-2002; 2002JP-00129046.
PR
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX
XX Shitara K, Nakamura K, Furuya A, Niwa R, Ohki Y, Hanai N;
PI
XX
XX WPI; 2003-854482/79.
DR

DR N-PSDB; ADJ95625.
XX
XX Antibodies and antibody fragments recognizing human insulin-like growth
PT factor for treatment and diagnosis of cancer, diabetes and rheumatoid
PT arthritis.
XX
XX Claim 6; SEQ ID NO 2; 115bp; Japanese.
PS
XX
XX The invention comprises antibodies and antibody fragments which bind to
CC and inhibit the function of human insulin-like growth factor (IGF-I
CC and/or IGF-II). The antibodies and antibody fragments of the invention
CC are useful for the treatment, prevention, and diagnosis of diabetes,
CC rheumatoid arthritis and cancer. The present amino acid sequence
CC represents a rat insulin-like growth factor-related protein of the
CC invention.
XX
XX
SQ Sequence 137 AA;

Query Match 83.1%; Score 74; DB 7; Length 137;
Best Local Similarity 82.4%; Pred. No. 0.0059;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGCTYYSDSVKG 17
DB 69 YISSGGSGCTYYRDSVKG 85

RESULT 21
ADG25805
ID ADG25805 standard; protein; 117 AA.
XX
XX ADG25805;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Anti-CD30 monoclonal antibody VH variable region T14 SEQ ID NO:5.
DE
XX
XX antibody; CD30; anti-CD30 antibody; cytostatic; gene therapy; cancer.
KW
XX
XX Synthetic.
OS
XX
XX WO2003104432-A2.
PN
XX
XX 18-DEC-2003.
PD
XX
XX 09-JUN-2003; 2003WO-US018373.
PF
XX
XX 07-JUN-2002; 2002US-0387293P.
PR
XX
XX 16-SEP-2002; 2002US-0411032P.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Pastan IH, Nagata S, Onda M, Numata Y, Santora K, Beers R;
PI
XX
XX Kretzman R, Sinha A;
PI
XX
XX WPI; 2004-062352/06.
DR
XX
XX New antibody that binds specifically to a stalk of CD30 of a cell, or to
PT an epitope destroyed upon cleavage of soluble CD30 (sCD30) from intact
PT CD30, useful for inhibiting the growth of a CD30+ cancer cell.
PT
XX
XX Example 1; SEQ ID NO 5; 102bp; English.
PS
XX
XX The present invention describes an isolated antibody that binds
CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed
CC upon cleavage of soluble CD30 (sCD30) from intact CD30. Also described:
CC (1) a composition comprising the antibody conjugated or fused to a
CC therapeutic part; (2) a nucleic acid encoding an antibody that binds
CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed
CC upon cleavage of sCD30 from intact CD30; (3) an expression vector
CC comprising the nucleic acid operably linked to a promoter; (4) inhibiting
CC growth of a CD30+ cancer cell; (5) detecting the presence of a CD30+ cell
CC in a biological sample; (6) a host cell expressing the isolated nucleic

CC acid encoding the antibody having variable heavy and variable light
CC chains; and (7) a kit for detecting the presence of a CD30+ cancer cell
CC in a biological sample comprising a container and an anti-CD30 antibody.
CC An anti-CD30 antibody has cytostatic activity, and can be used in gene
CC therapy. The anti-CD30 antibody that binds specifically to a stalk of
CC CD30 of a cell, or to an epitope destroyed upon cleavage of scd30 from
CC intact CD30 is useful for the manufacture of a medicament for inhibiting
CC the growth of a CD30+ cancer cell. The present sequence is used in the
CC exemplification of the present invention.

CC
XX
SQ Sequence 117 AA;

Query Match 82.0%; Score 73; DB 8; Length 117;
Best Local Similarity 93.8%; Pred. No. 0.007;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ISSGGSGTYSYDSVKG 17
Db 51 ISSGGSGTYSYDSVKG 66

RESULT 22
ADC27437
ID ADC27437 standard; protein; 120 AA.
XX
AC ADC27437;
XX
DT 18-DEC-2003 (first entry)
XX
DE TMEFF2#10 heavy chain variable region SEQ ID NO:6.
XX
KM antibody; TMEFF2#19; TMEFF2; binding inhibitor; prostate cancer;
KM cytostatic; vaccine; primary prostate cancer; metastatic prostate cancer;
KM locally advanced prostate cancer; androgen independent prostate cancer.
XX
OS Synthetic.
XX
PN WO2003075855-A2.
XX
PD 18-SEP-2003.
XX
PE 07-MAR-2003; 2003WO-US007209.
XX
PR 08-MAR-2002; 2002US-0362837P.
XX
PR 27-DEC-2002; 2002US-0436812P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Bhaskar V, De la Calle A, Law D, Caras I, Ramakrishnan V;
PI Murray R, Afar D, Powers D;
PI N-PSDB; ADC27436.
XX
DR WPI; 2003-756783/71.
XX
PT New antibody that competitively inhibits binding of TMEFF219 to TMEFF2,
PT useful for treating prostate cancer, e.g. primary, metastatic, locally
PT advanced, or androgen independent prostate cancer.
XX
PS Example 1; SEQ ID NO 6; 51pp; English.

CC The present invention describes an antibody (1) that competitively
CC inhibits binding of TMEFF2#19 to TMEFF2. Also described: (1) a
CC pharmaceutical composition comprising the antibody and a carrier; (2)
CC detecting a prostate cancer cell in a biological sample from a patient by
CC contacting the biological sample with the antibody; (3) inhibiting
CC proliferation of a prostate cancer-associated cell by contacting the cell
CC with the antibody; and (4) treating prostate cancer with an antibody to
CC TMEFF2. (1) has cytostatic activity and can be used in vaccines. The
CC antibody, composition and method are useful for treating prostate cancer,
CC e.g. primary prostate cancer, metastatic prostate cancer, locally
CC advanced prostate cancer, androgen independent prostate cancer, prostate
CC cancer that has been treated with neoadjuvant therapy, or prostate cancer
CC that is refractory to treatment with neoadjuvant therapy. The present

CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 120 AA;

Query Match 82.0%; Score 73; DB 7; Length 120;
Best Local Similarity 76.5%; Pred. No. 0.0072;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 YISSGGSGTYSYDSVKG 17
Db 50 YISSGGSGTYSYDSVKG 66

RESULT 23
ABP46028
ID ABP46028 standard; protein; 237 AA.
XX
AC ABP46028;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 2039.
XX
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PE 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
XX
PR 17-OCT-2000; 2000US-0240816P.
XX
PR 16-MAR-2001; 2001US-0276248P.
XX
PR 21-MAR-2001; 2001US-0277379P.
XX
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI WPI; 2002-114799/15.
XX
DR
XX
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2831-2832; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention

Sequence 237 AA;
Query Match 80.9%; Score 72; DB 7; Length 237;
Best Local Similarity 82.4%; Pred. No. 0.021;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGSGSTYYSDSVK 17
|||||
50 YISSGSGSTYYADSVK 66

DB 50 YISSGSGSTYYADSVK 66

RESULT 26
ADG96855
ID ADG96855 standard; protein; 237 AA.
AC ADG96855;
XX
XX 11-MAR-2004 (first entry)
DE Single chain antibody that immunospecifically binds Blys SeqID 2039.
XX
XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX B cell proliferation; differentiation; scfv; myasthenia gravis;
XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
XX antinflammatory; antiasthmatic; antiallergic; cytostatic.
OS Unidentified.
XX
XX MO2003055979-A2.
XX
XX 10-JUL-2003.
XX
XX 14-NOV-2002; 2002WO-US036496.
XX
XX 16-NOV-2001; 2001US-0331469P.
XX 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
XX WPI, 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.
PS Example 1; SEQ ID NO 2039; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scfvs) derived, preferably, from the variable
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey Blys. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of Blys or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukaemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antineumatic, antiarthritic, neuroprotective,
XX antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
XX polypeptide sequence is a single chain antibody that binds Blys of the
XX invention. NOTE: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format
XX directly from Wipo at fcp.wipo.int/pub/published_pct_sequences.

Sequence 237 AA;
Query Match 80.9%; Score 72; DB 7; Length 237;
Best Local Similarity 82.4%; Pred. No. 0.021;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGSGSTYYSDSVK 17
|||||
50 YISSGSGSTYYADSVK 66

DB 50 YISSGSGSTYYADSVK 66

RESULT 27
ABP45894
ID ABP45894 standard; protein; 240 AA.
AC ABP45894;
XX
XX 19-AUG-2002 (first entry)
DE Human Blys binding scfv SEQ ID 1905.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
OS Homo sapiens.
XX
XX MO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI, 2002-114799/15.
XX
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
PS Claim 1; Page 2674-2675; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
XX Sequence 240 AA;

XX DE Variable region of murine AHT 54 heavy chain.
 XX XX Interleukin-2 receptor; Il-2; tumour necrosis factor; TNF; ss.
 XX OS Mus sp.
 XX PN EP380068-A.
 XX PD 01-AUG-1990.
 XX PF 24-JUN-1990; 90EP-00101351.
 XX PR 24-JAN-1989; 89US-00301216.
 XX PR 04-DEC-1989; 89US-00441702.
 XX PA (MOLE-) MOLECULAR THERAPY.
 XX PI Zerler B;
 XX DR WPI; 1990-232892/31.
 XX DR N-PSDB; AAQ05555.
 XX PS Disclosure; Page ?; -PP; English.
 XX CC Mabs comprising mouse CH and CL constant regions with human variable
 CC regions may be used to create mouse/human hybrid Mabs, which have a
 CC longer serum half-life. Method can be used to produce Abs against
 CC Interleukin-2 receptor and tumour necrosis factor
 XX SQ Sequence 136 AA;
 QY 1 YISGSGGTYYSDSVKG 17
 Db 69 YISGSGDNTYPPDVKG 85
 Query Match 79.8%; Score 71; DB 2; Length 136;
 Best Local Similarity 76.5%; Pred. No. 0.016;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 RESULT 31
 AAP80156
 ID AAP80156 standard; protein; 247 AA.
 XX AC AAP80156;
 XX DT 31-OCT-2002 (revised)
 DT 14-NOV-1990 (first entry)
 XX DE Biosynthetic antibody binding site.
 XX DE Biosynthetic antibody binding site.
 XX KW Biosynthetic antibody binding site; framework region; assay; imaging;
 KW multifunctional protein.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO8809344-A.
 XX PD 01-DEC-1988.
 XX PF 19-MAY-1988; 88WO-US001737.
 XX PR 21-MAY-1987; 87US-00052800.
 XX PA (CREA-) CREATIVE BIOMOLECULES INC.
 XX PI Huston J, Oppermann H;
 XX

DR WPI; 1988-353928/49.
 DR N-PSDB; AAN80182.
 XX PT Recombinant multifunctional protein - having an antibody binding site and
 PT a sequence for biological activity, ion sequestering or binding to a
 PT solid support.
 XX PS Disclosure; Page ?; 15pp; English.
 XX CC The biosynthetic antibody binding site forms part of a recombinant
 CC multifunctional protein which also comprises an effector protein, an AA
 CC sequence capable of sequestering an ion, or a sequence capable of binding
 CC to a solid support. The BABS comprises framework regions in both VH and
 CC LH and CDR1 and CDR3 in VH, and CDR1, CDR2 and CDR3 in VL from an anti-
 CC CEA monoclonal antibody. CDR2 in VH is a CDR2 consensus sequence found in
 CC most immunoglobulin VH regions. The effector protein is an enzyme, toxin,
 CC receptor, binding site, growth factor, cytokine or antimetabolite. The
 CC sequence capable of sequestering an ion is calmodulin or metallothionein.
 CC The sequence able to bind to a solid support is streptavidin or a protein
 CC A fragment. The protein may be used for, eg specific binding assays,
 CC affinity purification, biocatalysis, drug targeting, imaging and
 CC immunological treatment of oncogenic and infectious diseases. The protein
 CC offers fewer cleavage sites to circulating proteolytic enzymes and have
 CC improved stability. They reach target organs rapidly and are cleared
 CC quickly from the body. They also have reduced immunogenicity. (Updated on
 CC 31-OCT-2002 to add missing OS field.)
 XX SQ Sequence 247 AA;
 QY 2 ISSGSGGTYYSDSVKG 17
 Db 53 ISSGSGDNTYPPDVKG 68
 Query Match 79.8%; Score 71; DB 1; Length 247;
 Best Local Similarity 87.5%; Pred. No. 0.03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 RESULT 32
 AAB20436
 ID AAB20436 standard; protein; 249 AA.
 XX AC AAB20436;
 XX DT 21-JUN-2001 (first entry)
 XX DE Anti-FIX/FIXa antibody 198/A1 scFv.
 XX KW Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 KW haemorrhagic diathesis; haemostatic; amidiolytic; therapy; mouse.
 XX OS Mus musculus.
 OS Synthetic.
 OS Chimeric.
 XX FH Key
 FT Protein 1.122
 FT /label= VH
 FT Region 99.111
 FT /label= CDR3
 FT Peptide 123.136
 FT /label= Linker
 FT Protein 137.249
 FT /label= VL
 FT Misc-difference 142
 FT /note= "encoded by ACN"
 FT Misc-difference 224
 FT /note= "encoded by GCN"
 FT Region 230.238
 FT /label= CDR3
 XX PN WO200119992-A2.


```

FT      Protein      /label= Signal_peptide
FT      PT           23..294
FT      PT           /label= Mature_protein
FT      PT           23..271
FT      PT           /label= scFv
FT      PT           23..144
FT      PT           /label= VH
FT      PT           Misc-difference 76
FT      PT           /note= "encoded by GGN"
FT      PT           Peptide      145..159
FT      PT           /label= Linker
FT      PT           Region      150..271
FT      PT           /label= VL
FT      PT           Peptide      272..274
FT      PT           /label= Spacer
FT      PT           Protein      275..286
FT      PT           /label= Myc_tag
FT      PT           Peptide      287..288
FT      PT           /label= Spacer
FT      PT           Peptide      289..294
FT      PT           /label= His_tag

PN      MO20011992-A2.
XX      PD           22-MAR-2001.
XX      PF           13-SEP-2000; 2000MO-EP008936.
XX      PR           14-SEP-1999; 99AT-00001576.
XX      PA           (BAXT ) BAXTER AG.
XX      PI           Scheiflinger F, Kerschbaumer R, Falkner F, Dörner F,
XX      PI           N-PSDB; AAF30732.
XX      PT           WPI; 2001-290358/30.
XX      PT           New factor IX/factor IXa antibodies and their derivatives useful for
XX      PT           increasing amidolytic activity of factor IXa, and for treating blood
XX      PT           coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX      PS           Example 18; Fig 34; 138pp; English.

CC      The present sequence is that of a fusion protein comprising: a pelB
CC      leader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising
CC      the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by
CC      an artificial, flexible linker peptide; a spacer; a Myc-tag peptide; a
CC      spacer; and a C-terminal 6His affinity tail. 198/B1 is an example of anti-
CC      human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the
CC      invention. Anti-FIX/FIXa antibodies and their derivatives, including scFv
CC      fragments, have FIXa cofactor activity or FIXa activating activity.
CC      Administration leads to an increase in the procoagulant activity of FIXa,
CC      even in the presence of FVIIa inhibitors. This allows for rapid blood
CC      coagulation even in the absence of FVIII or FVIIa, and in the case of
CC      FVIII inhibitor patients. The antibodies and derivatives are used in a
CC      claimed pharmaceutical composition for treating patients with blood
CC      coagulation disorders, especially haemophilia A and haemorrhagic
CC      diathesis. The scFv-myc-tag fusion was expressed in E. coli. It exhibited
CC      FVIII-like activity
XX      CC
XX      SQ           Sequence 294 AA:

Query Match      79.8%; Score 71; DB 4; Length 294;
Best Local Similarity 87.5%; Pred. No. 0.037;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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ID      AAB20438 standard; protein; 325 AA.
XX      AC           AAB20438;
XX      XX           21-JUN-2001 (first entry)
XX      DT           Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody.
XX      DE           XX
XX      KW           Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
XX      KW           Factor VII cofactor; blood coagulation disorder; haemophilia A;
XX      KW           haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
XX      KW           bivalent antibody; plasmid pz19-198AB2#102.
XX      OS           Mus musculus.
XX      OS           Synthetic.
XX      OS           Escherichia coli.
XX      OS           Chimeric.
XX      FH           Key
XX      FT           Peptide      1..22
XX      FT           /label= Signal_peptide
XX      FT           /note= "pelB leader"
XX      FT           Protein      23..325
XX      FT           /label= Mature_protein
XX      FT           Protein      23..271
XX      FT           /label= scFv
XX      FT           Region      23..144
XX      FT           /label= VH
XX      FT           Misc-difference 76
XX      FT           /note= "encoded by GGN"
XX      FT           Peptide      145..159
XX      FT           /label= Linker
XX      FT           Region      160..271
XX      FT           /label= VL
XX      FT           Misc-difference 166
XX      FT           /note= "encoded by TN"
XX      FT           PT           Misc-difference 181
XX      FT           /note= "encoded by TCN"
XX      FT           Peptide      272..274
XX      FT           /label= Spacer
XX      FT           Protein      275..284
XX      FT           /label= Hinge
XX      FT           Protein      285..319
XX      FT           /label= Helix
XX      FT           Peptide      320..325
XX      FT           /label= His_tag

PN      MO20011992-A2.
XX      PD           22-MAR-2001.
XX      PF           13-SEP-2000; 2000MO-EP008936.
XX      PR           14-SEP-1999; 99AT-00001576.
XX      PA           (BAXT ) BAXTER AG.
XX      PI           Scheiflinger F, Kerschbaumer R, Falkner F, Dörner F,
XX      PI           N-PSDB; AAF30728.
XX      PT           WPI; 2001-290358/30.
XX      PT           New factor IX/factor IXa antibodies and their derivatives useful for
XX      PT           increasing amidolytic activity of factor IXa, and for treating blood
XX      PT           coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX      PS           Example 16; Fig 28; 138pp; English.

CC      The present sequence is that of a bivalent miniantibody comprising a pelB
CC      leader peptide, the single chain Fv (scFv) fragment of antibody 198/B1
CC      (subclone AB2), an amphipathic helical structure and a C-terminal 6His
CC      tag. The protein was expressed in Escherichia coli from plasmid
CC      pz1p198AB2#102 (see AAF30728). Antibody 198/B1 is an example of anti-

```

CC	human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the
CC	invention. Anti-FIX/FIXa antibodies and their derivatives have FVIIa
CC	cotactor activity or FIXa activating activity. Administration leads to an
CC	increase in the procoagulant activity of FIXa, even in the presence of
CC	FVIIa inhibitors. This allows for rapid blood coagulation even in the
CC	absence of FVIII or FVIIa, and in the case of FVIII inhibitor patients.
CC	The antibodies and derivatives are used in a claimed pharmaceutical
CC	composition for treating patients with blood coagulation disorders,
CC	especially haemophilia A and haemorrhagic diathesis. The bivalent
CC	monoclonal antibody exhibited FVIII-like activity
XX	
SO	Sequence 325 AA;
XX	
Query Match	79.8%; Score 71; DB 4; Length 325;
Best Local Similarity	87.5%; Pred. No. 0.041;
Matches 14; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	2 ISSGSGSTYYSDSVKG 17
DB	73 ISSGSGSTYYSDSVKG 88
XX	
RESULT 36	
AAB20437	
ID	AAB20437 standard; protein; 732 AA.
XX	
AC	AAB20437;
XX	
DT	21-JUN-2001 (first entry)
XX	
DE	Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion.
XX	
KM	Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KM	Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KM	haemorrhagic diathesis; haemostatic; amydolytic; therapy; mouse;
KM	alkaline phosphatase.
XX	
OS	Mus musculus.
OS	Synthetic.
OS	Escherichia coli.
OS	Chimeric.
XX	
FH	Key
FT	Peptide
FT	1..22
FT	/label=Signal_peptide
FT	23..732
FT	/label=Mature_protein
FT	23..271
FT	/label=scFv
FT	23..144
FT	/label=VH
FT	76
FT	Misc-difference
FT	/note="encoded by GGN"
FT	Peptide
FT	145..159
FT	/label=Linker
FT	160..271
FT	/label=VL
FT	272..275
FT	/label=Spacer
FT	276..725
FT	/label=Alkaline_phosphatase
FT	726..732
FT	Peptide
FT	/label=His_tag
XX	
PN	WO200119992-A2.
XX	
XX	22-MAR-2001.
XX	
PF	13-SEP-2000; 2000WO-EP008936.
XX	
PR	14-SEP-1999; 99AT-00001576.
XX	
BA	(BAXT) BAXTER AG.

XX	PI	Schneiflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX	XX	WPI; 2001-290358/30.
DR	N-PSDB; AAB30727.	
XX	XX	New factor IX/factor IXa antibodies and their derivatives useful for
PT	PT	increasing antidotolytic activity of factor IXa, and for treating blood
PT	PT	coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX	XX	
PS	PS	Example 16; Fig 26; 138pp; English.
XX	XX	
CC	CC	The present sequence is that of a fusion protein comprising: a pelB
CC	CC	leader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising
CC	CC	the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by
CC	CC	an artificial, flexible linker peptide; a spacer; Escherichia coli
CC	CC	alkaline phosphatase; and a C-terminal 6His affinity tail. 198/B1 is an
CC	CC	example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
CC	CC	antibodies of the invention. Anti-FIX/FIXa antibodies and their
CC	CC	derivatives, including scFv fragments, have FvIIa cofactor activity or
CC	CC	FIXa activating activity. Administration leads to an increase in the
CC	CC	procoagulant activity of FIXa, even in the presence of FvIIa inhibitors.
CC	CC	This allows for rapid blood coagulation even in the absence of FvIII or
CC	CC	FvIIa, and in the case of FvIII inhibitor patients. The antibodies and
CC	CC	derivatives are used in a claimed pharmaceutical composition for treating
CC	CC	patients with blood coagulation disorders, especially haemophilia A and
CC	CC	haemorrhagic diathesis. The scFv-alkaline phosphatase was expressed in E.
CC	CC	coli. It exhibited FvIII-like activity
XX	XX	
SQ	SQ	Sequence 732 AA;
		Query Match 79.8%; Score 71; DB 4; Length 732;
		Best Local Similarity 87.5%; Pred. No. 0.097;
		Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
Oy		
		2 ISSGSGTYYSDSYKG 17
Db		73 ISSGSGSTYYPSVXG 88
RESULT 37		
AAR82986		AAR82986 standard; protein; 119 AA.
XX	AC	
XX	XX	AAR82986;
XX	DT	22-MAR-1996 (first entry)
XX	DB	LK26 humanised VH region.
XX	XX	
KW	KW	LK26 antigen; humanised antibody; antibody engineering; CDR;
KM	KM	complementarily determining region; monoclonal antibody; heavy chain;
KV	KV	framework NEMM; cancer; diagnosis; LK26HuVH1, I.
XX	OS	Synthetic.
XX	XX	
FH	FH	Key Location/Qualifiers
FT	FT	Misc-difference 24 /note= "murine residue"
FT	FT	Misc-difference 27 /note= "murine residue"
FT	FT	Misc-difference 48.49 /note= "murine residues"
FT	FT	Misc-difference 72 /note= "murine residue"
FT	FT	Misc-difference 93 /note= "murine residue"
FT	FT	Misc-difference 95 /note= "murine residue"
XX	XX	
XX	XX	WO9524482-A1.
XX	XX	
XX	XX	14-SEP-1995.

```
XX 08-MAR-1995; 95WO-US003094.
XX 08-MAR-1994; 94US-00207996.
XX (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Wallace TP, Harris WJ, Carr FJ, Rettig WJ, Garin-Chesa P, Old LJ;
XX WPI; 1995-328273/42.
XX
XX Recombinant humanised anti-LK26 antibody - useful to treat and detect
XX cancer cells in a human.
XX
XX Example 1; Page 23; 45pp; English.
XX
XX A humanised heavy chain variable region (AAR82979), LK26HuVH, comprises
XX the human NEMM framework (with some additional murine framework residues
XX required for antigen specificity) and mouse complementarity determining
XX regions from a monoclonal antibody specific for the LK26 cancer antigen.
XX LK26HuVH and its variants (AAR82980-82, AAR82986) are used as components
XX of humanised anti-LK26 antibodies
XX
XX Sequence 119 AA;
SQ
Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.019;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 ISSGSGTYYSDSVKG 17
Db 51 ISSGSGTYYADSVKG 66
RESULT 38
AAR82980
ID AAR82980 standard; protein; 119 AA.
XX
XX AAR82980;
XX
XX 22-MAR-1996 (first entry)
XX
XX LK26 humanised VH region.
XX
XX LK26 antigen; humanised antibody; antibody engineering; CDR;
XX complementarity determining region; monoclonal antibody; heavy chain;
XX framework NEMM; cancer; diagnosis; LK26HuVH.F.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 24 /note= "murine residue"
XX FT Misc-difference 27 /note= "murine residue"
XX FT Misc-difference 48..49 /note= "murine residues"
XX FT Misc-difference 68..72 /note= "murine residues"
XX FT Misc-difference 74 /note= "murine residues"
XX FT /note= "murine residue"
XX
XX WO9524482-A1.
XX
XX 14-SEP-1995.
XX
XX 08-MAR-1995; 95WO-US003094.
XX
XX 08-MAR-1994; 94US-00207996.
XX
XX (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
XX (LUDW-) LUDWIG INST CANCER RES.
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XX Wallace TP, Harris WJ, Carr FJ, Rettig WJ, Garin-Chesa P, Old LJ;
XX WPI; 1995-328273/42.
XX
XX Recombinant humanised anti-LK26 antibody - useful to treat and detect
XX cancer cells in a human.
XX
XX Example 1; Page 23; 45pp; English.
XX
XX A humanised heavy chain variable region (AAR82979), LK26HuVH, comprises
XX the human NEMM framework (with some additional murine framework residues
XX required for antigen specificity) and mouse complementarity determining
XX regions from a monoclonal antibody specific for the LK26 cancer antigen.
XX LK26HuVH and its variants (AAR82980-82, AAR82986) are used as components
XX of humanised anti-LK26 antibodies
XX
XX Sequence 119 AA;
SQ
Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.019;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 ISSGSGTYYSDSVKG 17
Db 51 ISSGSGTYYADSVKG 66
RESULT 39
AAR82981
ID AAR82981 standard; protein; 119 AA.
XX
XX AAR82981;
XX
XX 22-MAR-1996 (first entry)
XX
XX LK26 humanised VH region.
XX
XX LK26 antigen; humanised antibody; antibody engineering; CDR;
XX complementarity determining region; monoclonal antibody; heavy chain;
XX framework NEMM; cancer; diagnosis; LK26HuVH.F.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 24 /note= "murine residue"
XX FT Misc-difference 27 /note= "murine residue"
XX FT Misc-difference 48..49 /note= "murine residues"
XX FT Misc-difference 72 /note= "murine residues"
XX FT Misc-difference 78..80 /note= "murine residues"
XX FT /note= "murine residue"
XX
XX WO9524482-A1.
XX
XX 14-SEP-1995.
XX
XX 08-MAR-1995; 95WO-US003094.
XX
XX 08-MAR-1994; 94US-00207996.
XX
XX (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Wallace TP, Harris WJ, Carr FJ, Rettig WJ, Garin-Chesa P, Old LJ;
XX WPI; 1995-328273/42.
XX
XX Recombinant humanised anti-LK26 antibody - useful to treat and detect
XX cancer cells in a human.
```

```
XX Example 1; Page 23; 45pp; English.
PS
CC A humanised heavy chain variable region (AAR82979), LK26HuVH, comprises
CC the human NEMM framework (with some additional murine framework residues
CC required for antigen specificity) and mouse complementarity determining
CC regions from a monoclonal antibody specific for the LK26 cancer antigen.
CC LK26HuVH and its variants (AAR82980-82, AAR82986) are used as components
CC of humanised anti-LK26 antibodies
XX
SQ Sequence 119 AA;

Query Match      78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.019;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 ISSGSGSTYYSDSVKG 17
        |||||:|||||
        51 ISSGSGSTYYADSVKG 66

Db

RESULT 40
AAR82982
ID AAR82982 standard; protein; 119 AA.
XX
AC AAR82982;
XX
DT 22-MAR-1996 (first entry)
XX
DE LK26 humanised VH region.
XX
KW LK26 antigen; humanised antibody; antibody engineering; CDR;
KW complementarity determining region; monoclonal antibody; heavy chain;
KW framework KOL; cancer; diagnosis; LK26KOLHuVH.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 24 /note= "murine residue"
FT Misc-difference 28 /note= "murine residue"
FT Misc-difference 69 /note= "murine residue"
FT Misc-difference 75 /note= "murine residue"
FT Misc-difference 75 /note= "murine residue"
XX
PN WO9524482-A1.
XX
PD 14-SEP-1995.
XX
PF 08-MAR-1995; 95WO-US003094.
XX
PR 08-MAR-1994; 94US-00207996.
XX
PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Wallace TP, Harris WJ, Carr FU, Rettig WJ, Garin-Chesa P, Old LJ;
XX WPI; 1995-328273/42.
XX
PT Recombinant humanised anti-LK26 antibody - useful to treat and detect
PT cancer cells in a human.
XX
PS Example 1; Page 23; 45pp; English.
XX
CC A humanised heavy chain variable region (AAR82979), LK26HuVH, comprises
CC the human NEMM framework (with some additional murine framework residues
CC required for antigen specificity) and mouse complementarity determining
CC regions from a monoclonal antibody specific for the LK26 cancer antigen.
CC LK26HuVH and its variants (AAR82980-82, AAR82986) are used as components
CC of humanised anti-LK26 antibodies
```

```
XX
SQ Sequence 119 AA;

Query Match      78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.019;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 ISSGSGSTYYSDSVKG 17
        |||||:|||||
        51 ISSGSGSTYYADSVKG 66

Db
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Search completed: December 17, 2004, 18:29:00
Job time : 53.6685 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 17, 2004, 18:13:27 ; Search time 10.3146 Seconds
(without alignments)
109.302 Million cell updates/sec

Title: US-10-089-500-4

Perfect score: 89

Sequence: 1 YISSGSGGTYSDSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:*
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4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
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6: /cgn2_6/prodata/1/1aa/backfill1.pep:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	130	4	US-09-225-322B-18
2	89	100.0	130	4	US-09-764-304-18
3	82	92.1	130	4	US-09-225-322B-8
4	82	92.1	130	4	US-09-764-304-8
5	77	86.5	119	5	PCT-US94-07659-6
6	77	86.5	247	5	PCT-US94-07659-2
7	75	84.3	118	1	US-08-326-362-2
8	70	78.7	119	1	US-08-207-996-18
9	70	78.7	119	1	US-08-207-996-19
10	70	78.7	119	1	US-08-207-996-20
11	70	78.7	119	1	US-08-207-996-21
12	70	78.7	119	1	US-08-207-996-22
13	70	78.7	119	1	US-08-207-996-27
14	70	78.7	119	2	US-08-760-840A-18
15	70	78.7	119	2	US-08-760-840A-19
16	70	78.7	119	2	US-08-760-840A-20
17	70	78.7	119	2	US-08-760-840A-21
18	70	78.7	119	2	US-08-760-840A-22
19	70	78.7	119	2	US-08-760-840A-28
20	70	78.7	119	3	US-09-266-119-18
21	70	78.7	119	3	US-09-266-119-19
22	70	78.7	119	3	US-09-266-119-20
23	70	78.7	119	3	US-09-266-119-21
24	70	78.7	119	3	US-09-266-119-22
25	70	78.7	119	3	US-09-266-119-28
26	70	78.7	119	3	US-09-602-709-18
27	70	78.7	119	3	US-09-602-709-19

28	70	78.7	119	3	US-09-602-709-20	Sequence 20, Appl
29	70	78.7	119	3	US-09-602-709-21	Sequence 21, Appl
30	70	78.7	119	3	US-09-602-709-22	Sequence 22, Appl
31	70	78.7	119	3	US-09-602-709-28	Sequence 28, Appl
32	69	77.5	17	4	US-09-497-997C-31	Sequence 31, Appl
33	69	77.5	21	4	US-09-497-997C-19	Sequence 19, Appl
34	69	77.5	22	4	US-09-497-997C-4	Sequence 4, Appl1
35	69	77.5	22	4	US-09-497-997C-20	Sequence 20, Appl1
36	69	77.5	30	3	US-09-336-093-4	Sequence 4, Appl1
37	69	77.5	30	4	US-09-557-465D-4	Sequence 4, Appl1
38	69	77.5	30	4	US-09-497-997C-7	Sequence 7, Appl1
39	69	77.5	30	4	US-09-720-003C-5	Sequence 5, Appl1
40	69	77.5	31	4	US-09-497-997C-9	Sequence 9, Appl1
41	69	77.5	33	4	US-09-497-997C-23	Sequence 23, Appl1
42	69	77.5	49	4	US-09-497-997C-10	Sequence 10, Appl1
43	69	77.5	107	4	US-09-497-997C-26	Sequence 26, Appl1
44	68	76.4	87	4	US-09-840-459-53	Sequence 53, Appl1
45	68	76.4	87	4	US-09-497-625A-53	Sequence 53, Appl1

ALIGNMENTS

```
RESULT 1
US-09-225-322B-18
; Sequence 18, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA KM-641
US-09-225-322B-18

Query Match      100.0%; Score 89; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YISSGSGGTYSDSVKG 17
Db      60 YISSGSGGTYSDSVKG 76

RESULT 2
US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. 6435666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
```

```

; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIMAWA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA KM-641
US-09-764-304-18
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Query Match          100.0%; Score 89; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  YISSGSGTTYSDSVKG 17
          |||||
Db      60  YISSGSGTTYSDSVKG 76
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RESULT 3
US-09-225-322B-8
; Sequence 8, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIMAWA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-09-225-322B-8
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Query Match          92.1%; Score 82; DB 4; Length 130;
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Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2  ISSGSGTTYSDSVKG 17
          |||||
Db      61  ISSGSGTTYSDSVKG 76
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RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIMAWA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA KM-641
US-09-764-304-8
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Query Match          92.1%; Score 82; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2  ISSGSGTTYSDSVKG 17
          |||||
Db      61  ISSGSGTTYSDSVKG 76
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RESULT 5
PCT-US94-07659-6
; Sequence 6, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
```


COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match 86.5%; Score 77; DB 5; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YISSGGSGTYSDSVKG 17
DB 50 YISSGGSGTYSDSVKG 66

RESULT 6
PCT-US94-07659-2
Sequence 2, Application PC/TUS9407659
GENERAL INFORMATION:
APPLICANT: Young, Peter
APPLICANT: Gross, Mitchell
APPLICANT: Jonak, Zdenka L.
APPLICANT: Theisen, Timothy
APPLICANT: Hurle, Mark
APPLICANT: Jackson, Jeffrey R.
TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corp.
ADDRESSER: Intellectual Property
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 86.5%; Score 77; DB 5; Length 247;
Best Local Similarity 82.4%; Pred. No. 0.0021;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YISSGGSGTYSDSVKG 17
DB 69 YISSGGSGTYSDSVKG 85

RESULT 7
US-08-326-362-2
Sequence 2, Application US/08326362
Patent No. 5730981
GENERAL INFORMATION:
APPLICANT: Bogsiet, Klaus
APPLICANT: Seeman, Gerhard
APPLICANT: Dippold, Wolfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,362
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/032,863
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: DE P 42 08 795.3
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1276-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-326-362-2

Query Match 84.3%; Score 75; DB 1; Length 118;
Best Local Similarity 82.4%; Pred. No. 0.0019;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YISSGGSTYSDSVKG 17
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Db 50 YISSGASTYSDSVKG 66

RESULT 8

US-08-207-996-18
; Sequence 18, Application US/08207996
; Patent No. 5646253
; GENERAL INFORMATION:
; APPLICANT: Scotogen Biopharmaceuticals, Inc.
; APPLICANT: 1014 Hamilton Court
; APPLICANT: Menlo Park, California 94025
; APPLICANT: United States of America
; APPLICANT: 1345 Avenue of the Americas
; APPLICANT: New York, New York 10105
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.0/ASCII standard
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,996
; FILING DATE: 08-MAR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD-5363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-207-996-18

Query Match 78.7%; Score 70; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSTYSDSVKG 17
|||||:|||||
Db 51 ISSGGSTYSDSVKG 66

RESULT 9

US-08-207-996-19
; Sequence 19, Application US/08207996
; Patent No. 5646253
; GENERAL INFORMATION:
; APPLICANT: Scotogen Biopharmaceuticals, Inc.
; APPLICANT: 1014 Hamilton Court
; APPLICANT: Menlo Park, California 94025
; APPLICANT: United States of America
; APPLICANT: 1345 Avenue of the Americas

; APPLICANT: New York, New York 10105
; APPLICANT: United States of America
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.0/ASCII standard
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,996
; FILING DATE: 08-MAR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD-5363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-207-996-19

Query Match 78.7%; Score 70; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSTYSDSVKG 17
|||||:|||||
Db 51 ISSGGSTYSDSVKG 66

RESULT 10

US-08-207-996-20
; Sequence 20, Application US/08207996
; Patent No. 5646253
; GENERAL INFORMATION:
; APPLICANT: Scotogen Biopharmaceuticals, Inc.
; APPLICANT: 1014 Hamilton Court
; APPLICANT: Menlo Park, California 94025
; APPLICANT: United States of America
; APPLICANT: 1345 Avenue of the Americas
; APPLICANT: New York, New York 10105
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.0/ASCII standard

MOLECULE TYPE: DNA (genomic)
US-08-207-996-21
Query Match
Best Local Similarity 78.7%; Score 70; DB 1; Length 119;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ISSGSGTYTYSVKG 17
Db 51 ISSGSGTYTYSVKG 66
RESULT 11
US-08-207-996-21
Sequence 21, Application US/08207996
Patent No. 5646253
GENERAL INFORMATION:
APPLICANT: Scotgen Biopharmaceuticals, Inc.
APPLICANT: 1014 Hamilton Court
APPLICANT: Menlo Park, California 94025
APPLICANT: United States of America
APPLICANT: 1345 Avenue of the Americas
APPLICANT: New York, New York 10105
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,996
FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-207-996-21
Query Match
Best Local Similarity 78.7%; Score 70; DB 1; Length 119;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ISSGSGTYTYSVKG 17
Db 51 ISSGSGTYTYSVKG 66
RESULT 12
US-08-207-996-22
Sequence 22, Application US/08207996
Patent No. 5646253
GENERAL INFORMATION:
APPLICANT: Scotgen Biopharmaceuticals, Inc.
APPLICANT: 1014 Hamilton Court
APPLICANT: Menlo Park, California 94025
APPLICANT: United States of America
APPLICANT: 1345 Avenue of the Americas
APPLICANT: New York, New York 10105
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,996
FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-207-996-22
Query Match
Best Local Similarity 78.7%; Score 70; DB 1; Length 119;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ISSGSGTYTYSVKG 17
Db 51 ISSGSGTYTYSVKG 66
RESULT 13
US-08-207-996-27
Sequence 27, Application US/08207996
Patent No. 5646253
GENERAL INFORMATION:

APPLICANT: Scotgen Biopharmaceuticals, Inc.
APPLICANT: 1014 Hamilton Court
APPLICANT: Menlo Park, California 94025
APPLICANT: United States of America
APPLICANT: 1345 Avenue of the Americas
APPLICANT: New York, New York 10105
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
NUMBER OF SEQUENCES: 29
TITLE OF INVENTION: ANTIBODIES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,996
FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-207-996-27

Query Match 78.7%; Score 70; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGSTYSDSVKG 17
Db 51 ISSGSGSTYADSVKG 66

RESULT 14
US-08-760-840A-18
Sequence 18, Application US/08760840A
Patent No. 5952484
GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARCIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
TELECOMMUNICATION INFORMATION:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884

SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
MOLECULE TYPE: protein
US-08-760-840A-18

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGSTYSDSVKG 17
Db 51 ISSGSGSTYADSVKG 66

RESULT 15
US-08-760-840A-19
Sequence 19, Application US/08760840A
Patent No. 5952484
GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARCIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
TELECOMMUNICATION INFORMATION:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884

INFORMATION FOR SEQ ID NO: 19;
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-760-840A-19

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096; 1; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 1;

QY 2 ISSGSGTYSDSVKG 17
DB 51 ISSGSGTYTADSVKG 66

RESULT 16
US-08-760-840A-20
Sequence 20, Application US/08760840A
Patent No. 5952484

GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCES/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-760-840A-20

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096; 1; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 1;

QY 2 ISSGSGTYSDSVKG 17
DB 51 ISSGSGTYTADSVKG 66

RESULT 17
US-08-760-840A-21
Sequence 21, Application US/08760840A
Patent No. 5952484

GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCES/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-760-840A-21

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096; 1; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 1;

QY 2 ISSGSGTYSDSVKG 17
DB 51 ISSGSGTYTADSVKG 66

RESULT 18
US-08-760-840A-22
Sequence 22, Application US/08760840A
Patent No. 5952484

GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch

STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-760-840A-22

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 51 ISSGSGTYYSDSVKG 66

RESULT 19
US-08-760-840A-28
Sequence 28, Application US/08760840A
Patent No. 5952484
GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 95/03094

FILING DATE: 08-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-760-840A-28

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 51 ISSGSGTYYSDSVKG 66

RESULT 20
US-09-266-119-18
Sequence 18, Application US/09266119
Patent No. 6124106
GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,119
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,840
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6124106man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein

US-09-266-119-18

Query Match 78.7%; Score 70; DB 3; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
|||||
Db 51 ISSGSGTYYADSVKG 66

RESULT 21

US-09-266-119-19
; Sequence 19, Application US/09266119
; Patent No. 6124106

GENERAL INFORMATION:

APPLICANT: PAUL WALLACE;
APPLICANT: WILLIAM J. HARRIS;
APPLICANT: WOLFGANG J. RETTIG;
APPLICANT: PILAR GARIN-CHESA;
APPLICANT: LLOYD J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,119

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/760,840

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6124106man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH

TELEPHONE: 212-688-9200

TELEFAX: 212-838-3884

INFORMATION FOR SEQ. ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-266-119-19

QY 2 ISSGSGTYYSDSVKG 17
|||||
Db 51 ISSGSGTYYADSVKG 66

RESULT 22

US-09-266-119-20
; Sequence 20, Application US/09266119
; Patent No. 6124106
; GENERAL INFORMATION:

APPLICANT: PAUL WALLACE;
APPLICANT: WILLIAM J. HARRIS;
APPLICANT: WOLFGANG J. RETTIG;
APPLICANT: PILAR GARIN-CHESA;
APPLICANT: LLOYD J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,119
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,840
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6124106man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ. ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein

US-09-266-119-20

Query Match 78.7%; Score 70; DB 3; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
|||||
Db 51 ISSGSGTYYADSVKG 66

RESULT 23

US-09-266-119-21
; Sequence 21, Application US/09266119
; Patent No. 6124106

GENERAL INFORMATION:

APPLICANT: PAUL WALLACE;
APPLICANT: WILLIAM J. HARRIS;
APPLICANT: WOLFGANG J. RETTIG;
APPLICANT: PILAR GARIN-CHESA;
APPLICANT: LLOYD J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Wordperfect
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/266,119
 ? FILING DATE:
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/760,840
 ? FILING DATE:
 ? CLASSIFICATION:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Hanson, No. 6124106man D.
 ? REGISTRATION NUMBER: 30,946
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 212-688-9200
 ? TELEFAX: 212-838-3884
 ? INFORMATION FOR SEQ ID NO: 21:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 119 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: unknown
 ? TOPOLOGY: unknown
 ? MOLECULE TYPE: protein
 ? US-09-266-119-21

Query Match 78.7%; Score 70; DB 3; Length 119;
 Best Local Similarity 87.5%; Pred. No. 0.0096;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
 DB 51 ISSGSGTYYADSVKG 66

? RESULT 24
 ? US-09-266-119-22
 ? Sequence 22, Application US/09266119
 ? Patent No. 6124106
 ? GENERAL INFORMATION:
 ? APPLICANT: Paul WALLACE;
 ? APPLICANT: William J. HARRIS;
 ? APPLICANT: Wolfgang J. RETTIG;
 ? APPLICANT: Pilar GARIN-CHESA;
 ? APPLICANT: Lloyd J. OLD
 ? TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
 ? NUMBER OF SEQUENCES: 31
 ? CLASSIFICATION:
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Felte & Lynch
 ? STREET: 805 Third Avenue
 ? CITY: New York
 ? STATE: New York
 ? COUNTRY: U.S.A.
 ? ZIP: 10022
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Wordperfect
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/266,119
 ? FILING DATE:
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/760,840
 ? FILING DATE:
 ? CLASSIFICATION:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Hanson, No. 6124106man D.
 ? REGISTRATION NUMBER: 30,946
 ? TELECOMMUNICATION INFORMATION:
 ? LUD 5363.1 DIV. - JEL/NDH/SLH
 ? TELECOMMUNICATION INFORMATION:

? TELEPHONE: 212-688-9200
 ? TELEFAX: 212-838-3884
 ? INFORMATION FOR SEQ ID NO: 22:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 119 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: unknown
 ? TOPOLOGY: unknown
 ? MOLECULE TYPE: protein
 ? US-09-266-119-22

Query Match 78.7%; Score 70; DB 3; Length 119;
 Best Local Similarity 87.5%; Pred. No. 0.0096;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
 DB 51 ISSGSGTYYADSVKG 66

? RESULT 25
 ? US-09-266-119-28
 ? Sequence 28, Application US/09266119
 ? Patent No. 6124106
 ? GENERAL INFORMATION:
 ? APPLICANT: Paul WALLACE;
 ? APPLICANT: William J. HARRIS;
 ? APPLICANT: Wolfgang J. RETTIG;
 ? APPLICANT: Pilar GARIN-CHESA;
 ? APPLICANT: Lloyd J. OLD
 ? TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
 ? NUMBER OF SEQUENCES: 31
 ? CLASSIFICATION:
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Felte & Lynch
 ? STREET: 805 Third Avenue
 ? CITY: New York
 ? STATE: New York
 ? COUNTRY: U.S.A.
 ? ZIP: 10022
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Wordperfect
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/266,119
 ? FILING DATE:
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/760,840
 ? FILING DATE:
 ? CLASSIFICATION:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Hanson, No. 6124106man D.
 ? REGISTRATION NUMBER: 30,946
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 212-688-9200
 ? TELEFAX: 212-838-3884
 ? INFORMATION FOR SEQ ID NO: 28:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 119 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: unknown
 ? TOPOLOGY: unknown
 ? MOLECULE TYPE: protein
 ? US-09-266-119-28

Db 51 ISSGSGSTYYADSVKG 66

RESULT 25

US-09-602-709-18

Sequence 18, Application US/09602709

Patent No. 6348195

GENERAL INFORMATION:

APPLICANT: Paul WALLACE;

William J. HARRIS;

Wolfgang J. RETTIG;

Pilar GARIN-CHESA;

Lloyd J. OLD

TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/602,709

FILING DATE: 26-Jun-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/266,119

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6348195man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-688-9200

TELEFAX: 212-838-3884

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-602-709-18

Query Match 78.7%, Score 70, DB 3, Length 119,

Best Local Similarity 87.5%, Pred. No. 0.0096,

Matches 14, Conservative 1, Mismatches 1, Indels 0, Gaps 0,

QY 2 ISSGSGSTYYADSVKG 17

Db 51 ISSGSGSTYYADSVKG 66

RESULT 27

US-09-602-709-19

Sequence 19, Application US/09602709

Patent No. 6348195

GENERAL INFORMATION:

APPLICANT: Paul WALLACE;

William J. HARRIS;

Wolfgang J. RETTIG;

Pilar GARIN-CHESA;

Lloyd J. OLD

TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/602,709

FILING DATE: 26-Jun-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/266,119

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6348195man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-688-9200

TELEFAX: 212-838-3884

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-602-709-19

Query Match 78.7%, Score 70, DB 3, Length 119,

Best Local Similarity 87.5%, Pred. No. 0.0096,

Matches 14, Conservative 1, Mismatches 1, Indels 0, Gaps 0,

QY 2 ISSGSGSTYYADSVKG 17

Db 51 ISSGSGSTYYADSVKG 66

RESULT 28

US-09-602-709-20

Sequence 20, Application US/09602709

Patent No. 6348195

GENERAL INFORMATION:

APPLICANT: Paul WALLACE;

William J. HARRIS;

Wolfgang J. RETTIG;

Pilar GARIN-CHESA;

Lloyd J. OLD

TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/602,709

FILING DATE: 26-Jun-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/266,119
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6348195man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-602-709-20

Query Match 78.7%; Score 70; DB 3; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
|||||:|||||
Db 51 ISSGSGTYYADSVKG 66

RESULT 29
US-09-602-709-21
Sequence 21, Application US/09602709
Patent No. 6348195
GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
William J. HARRIS;
Wolfgang J. RETTIG;
Pilar GARIN-CHESA;
Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/602,709
FILING DATE: 26-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/266,119
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6348195man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-602-709-21

Query Match 78.7%; Score 70; DB 3; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
|||||:|||||
Db 51 ISSGSGTYYADSVKG 66

RESULT 30
US-09-602-709-22
Sequence 22, Application US/09602709
Patent No. 6348195
GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
William J. HARRIS;
Wolfgang J. RETTIG;
Pilar GARIN-CHESA;
Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/602,709
FILING DATE: 26-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/266,119
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6348195man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-602-709-22

Query Match 78.7%; Score 70; DB 3; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
|||||:|||||
Db 51 ISSGSGTYYADSVKG 66

RESULT 31
US-09-602-709-28
Sequence 28, Application US/09602709

Patent No. 6348195
GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
William J. HARRIS;
Wolfgang J. RETTIG;
Pilar GARTIN-CHESA;
Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Peife & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/602,709
FILING DATE: 26-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/266,119
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6348195man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-602-709-28
Query Match 78.7%; Score 70; DB 3; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0096;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 ISSGGSGTYSDSVKG 17
Db 51 ISSGGSGTYSDSVKG 66
RESULT 32
US-09-497-997C-31
Sequence 31, Application US/09497997C
Patent No. 6635248
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/09/497,997C
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-497-997C-19
Query Match 77.5%; Score 69; DB 4; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.0018;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 YISRGVSTYSDTVKG 17
Db 1 YISRGVSTYSDTVKG 17
RESULT 33
US-09-497-997C-19
Sequence 19, Application US/09497997C
Patent No. 6635248
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO CI
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/09/497,997C
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-497-997C-19
Query Match 77.5%; Score 69; DB 4; Length 21;
Best Local Similarity 76.5%; Pred. No. 0.0023;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 YISGGSGTYSDSVKG 17
Db 3 YISRGVSTYSDTVKG 19
RESULT 34
US-09-497-997C-4
Sequence 4, Application US/09497997C
Patent No. 6635248
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPETO, DONATO

PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 31
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-497-997C-31
Query Match 77.5%; Score 69; DB 4; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.0018;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 YISGGSGTYSDSVKG 17
Db 1 YISRGVSTYSDTVKG 17
RESULT 33
US-09-497-997C-19
Sequence 19, Application US/09497997C
Patent No. 6635248
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO CI
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/09/497,997C
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-497-997C-19
Query Match 77.5%; Score 69; DB 4; Length 21;
Best Local Similarity 76.5%; Pred. No. 0.0023;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 YISGGSGTYSDSVKG 17
Db 3 YISRGVSTYSDTVKG 19
RESULT 34
US-09-497-997C-4
Sequence 4, Application US/09497997C
Patent No. 6635248
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPETO, DONATO

```

; TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
; FILE REFERENCE: 0660-0166-0XCONT
; CURRENT APPLICATION NUMBER: US/09/497,997C
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: PCT/FR98/01740
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
; US-09-497-997C-4

Query Match      77.5%; Score 69; DB 4; Length 22;
Best Local Similarity 76.5%; Pred. No. 0.0024;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 YISGGSGTYSYSDVKG 17
      ||| ||| ||| ||| |||
Db      3 YISRGGVSTYSYSDTVKG 19

RESULT 35
; US-09-497-997C-20
; Sequence 20, Application US/09497997C
; Patent No. 6635248
; GENERAL INFORMATION:
; APPLICANT: TERNYNCK, THERESA
; APPLICANT: AVRAMEAS, ALEXANDRE
; APPLICANT: BUTTIN, GERARD
; APPLICANT: AVRAMEAS, STRAITIS
; APPLICANT: SARON, MARIE-FRANCOISE
; APPLICANT: BLONDEL, BRUNO
; APPLICANT: COUDERC, THERESA
; APPLICANT: MICHELSON, SUSAN
; APPLICANT: ZIPETO, DONATO
; TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
; FILE REFERENCE: 0660-0166-0XCONT
; CURRENT APPLICATION NUMBER: US/09/497,997C
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: PCT/FR98/01740
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
; US-09-497-997C-20

Query Match      77.5%; Score 69; DB 4; Length 22;
Best Local Similarity 76.5%; Pred. No. 0.0024;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 YISGGSGTYSYSDVKG 17
      ||| ||| ||| ||| |||
Db      3 YISRGGVSTYSYSDTVKG 19

RESULT 36
; US-09-336-093-4
; Sequence 4, Application US/09336093A
; Patent No. 6348185
; GENERAL INFORMATION:
; APPLICANT: Washington University School of Medicine
; APPLICANT: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL
; TITLE OF INVENTION: IMAGING, DIAGNOSTICS, AND PHARMACEUTICAL THERAPY
; FILE REFERENCE: WSHU 2001
```

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; CURRENT APPLICATION NUMBER: US/09/336,093A
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; OTHER INFORMATION: derivable from the heavy chain variable region of
; OTHER INFORMATION: an anti-DNA monoclonal antibody
; US-09-336-093-4

Query Match      77.5%; Score 69; DB 3; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.0033;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 YISGGSGTYSYSDVKG 17
      ||| ||| ||| ||| |||
Db      3 YISRGGVSTYSYSDTVKG 19

RESULT 37
; US-09-557-465D-4
; Sequence 4, Application US/09557465D
; Patent No. 6589503
; GENERAL INFORMATION:
; APPLICANT: Washington University
; APPLICANT: Bivwica-Worms, David
; TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL IMAGING, DIAGNOSTI
; FILE REFERENCE: WSHU 2020
; CURRENT APPLICATION NUMBER: US/09/557,465D
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/557,465
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/336,093
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: US 60/090,087
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide derivable from the heavy chain variable region of an anti
; OTHER INFORMATION: -DNA monoclonal antibody
; US-09-557-465D-4

Query Match      77.5%; Score 69; DB 4; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.0033;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 YISGGSGTYSYSDVKG 17
      ||| ||| ||| ||| |||
Db      3 YISRGGVSTYSYSDTVKG 19

RESULT 38
; US-09-497-997C-7
; Sequence 7, Application US/09497997C
; Patent No. 6635248
; GENERAL INFORMATION:
; APPLICANT: TERNYNCK, THERESA
; APPLICANT: AVRAMEAS, ALEXANDRE
; APPLICANT: BUTTIN, GERARD
; APPLICANT: AVRAMEAS, STRAITIS
; APPLICANT: SARON, MARIE-FRANCOISE
; APPLICANT: BLONDEL, BRUNO
; APPLICANT: COUDERC, THERESA
```

APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPERO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/09/497,997C
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 7
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-497-997C-7

Query Match 77.5%; Score 69; DB 4; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.0033;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVKG 17
DB 3 YISRGVSTYSDTVKG 19

RESULT 39
US-09-720-003C-5

Sequence 5, Application US/09720003C
Patent No. 6740524
GENERAL INFORMATION:
APPLICANT: Akita, Teruo
APPLICANT: Yokoi, Haruhiko
APPLICANT: Okuyama, Hajime
APPLICANT: Takeda, Katsuo
APPLICANT: Hasegawa, Mamoru
APPLICANT: Nakanishi, Mahito
TITLE OF INVENTION: Nucleic Acid Transfer Phage
FILE REFERENCE: 50026/026001
CURRENT APPLICATION NUMBER: US/09/720,003C
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: PCT/JP99/03272
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: JP 10-189845
PRIOR FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 5
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially synthesized peptide sequence
US-09-720-003C-5

Query Match 77.5%; Score 69; DB 4; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.0033;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVKG 17
DB 3 YISRGVSTYSDTVKG 19

RESULT 40
US-09-497-997C-9

Sequence 9, Application US/09497997C
Patent No. 6635248
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD

APPLICANT: AVRAMEAS, STRATIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPERO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/09/497,997C
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 9
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-497-997C-9

Query Match 77.5%; Score 69; DB 4; Length 31;
Best Local Similarity 76.5%; Pred. No. 0.0033;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVKG 17
DB 4 YISRGVSTYSDTVKG 20

Search completed: December 17, 2004, 18:32:07
Job time : 10.3146 secs

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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:20:33 ; Search time 32.8539 Seconds
(without alignments)
185.159 Million cell updates/sec

Title: US-10-089-500-4

Perfect score: 89

Sequence: 1 YISGSGSGTYSYSDSVK 17

Scoring table: BLOSUM62

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications_AA.*
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9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	89	100.0	130	9	US-09-764-304-18
2	89	100.0	130	14	US-10-265-713-18
3	89	100.0	130	14	US-10-166-626-18
4	82	92.1	130	9	US-09-764-304-8
5	82	92.1	130	14	US-10-265-713-8
6	82	92.1	130	14	US-10-166-626-8
7	74	83.1	240	16	US-10-779-461-23
8	72	82.0	120	15	US-10-383-447-6
9	72	80.9	237	10	US-09-880-748-1906
10	72	80.9	237	10	US-09-880-748-2039
11	72	80.9	237	14	US-10-293-418-1906
12	72	80.9	237	14	US-10-293-418-2039
13	72	80.9	240	10	US-09-880-748-1905

14	72	80.9	240	14	US-10-293-418-1905	Sequence 1905, Ap
15	70	78.7	121	14	US-10-447-331-4	Sequence 31, Appl
16	69	77.5	17	14	US-10-460-471-31	Sequence 4, Appl
17	69	77.5	21	14	US-10-460-471-19	Sequence 19, Appl
18	69	77.5	22	14	US-10-460-471-19	Sequence 20, Appl
19	69	77.5	22	14	US-10-460-471-20	Sequence 7, Appl
20	69	77.5	30	14	US-10-460-471-7	Sequence 21, Appl
21	69	77.5	30	14	US-10-144-549-21	Sequence 4, Appl
22	69	77.5	30	14	US-10-368-280-4	Sequence 9, Appl
23	69	77.5	30	14	US-10-374-035-4	Sequence 23, Appl
24	69	77.5	31	14	US-10-460-471-9	Sequence 10, Appl
25	69	77.5	33	14	US-10-460-471-23	Sequence 26, Appl
26	69	77.5	49	14	US-10-460-471-10	Sequence 2, Appl
27	69	77.5	107	14	US-10-460-471-26	Sequence 26, Appl
28	69	77.5	123	10	US-09-892-613C-2	Sequence 9, Appl
29	69	77.5	140	13	US-10-006-773-4	Sequence 26, Appl
30	68	76.4	17	14	US-10-281-479A-26	Sequence 53, Appl
31	68	76.4	17	14	US-10-275-180A-26	Sequence 26, Appl
32	68	76.4	17	14	US-10-286-132A-26	Sequence 26, Appl
33	68	76.4	17	14	US-10-477-377-9	Sequence 53, Appl
34	68	76.4	87	9	US-09-840-459-53	Sequence 53, Appl
35	68	76.4	87	16	US-10-766-773-53	Sequence 53, Appl
36	68	76.4	87	16	US-10-766-773-53	Sequence 53, Appl
37	68	76.4	87	16	US-10-733-561-53	Sequence 49, Appl
38	68	76.4	89	9	US-09-840-459-49	Sequence 49, Appl
39	68	76.4	89	16	US-10-766-773-49	Sequence 49, Appl
40	68	76.4	89	16	US-10-766-610-49	Sequence 49, Appl
41	68	76.4	89	16	US-10-733-563-49	Sequence 38, Appl
42	68	76.4	98	9	US-09-840-459-38	Sequence 39, Appl
43	68	76.4	98	9	US-09-840-459-39	Sequence 41, Appl
44	68	76.4	98	9	US-09-840-459-41	Sequence 38, Appl
45	68	76.4	98	16	US-10-766-773-38	

ALIGNMENTS

RESULT 1
US-09-764-304-18.
Sequence 18, Application us/09764304
Patent No. US2002026036A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KIWANA, YOSHITSA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,332
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CDNA KM-641
US-09-764-304-18

Query Match 100.0%; Score 89; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISSGSGGTYYSDSVKG 17
DB 60 YISSGSGGTYYSDSVKG 76

RESULT 2
US-10-265-713-18
; Sequence 18, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA KM-641
US-10-265-713-18

Query Match 100.0%; Score 89; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISSGSGGTYYSDSVKG 17
DB 60 YISSGSGGTYYSDSVKG 76

RESULT 3
US-10-166-626-18
; Sequence 18, Application US/10166626
; Publication No. US2003016876A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133

; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA KM-641
US-10-166-626-18

Query Match 100.0%; Score 89; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISSGSGGTYYSDSVKG 17
DB 60 YISSGSGGTYYSDSVKG 76

RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA KM-641
US-09-764-304-8

Query Match 92.1%; Score 82; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISSGSGGTYYSDSVKG 17
DB 61 ISSGSGGTYYSDSVKG 76

RESULT 5
US-10-265-713-8

Sequence 8, Application US/10265713
Publication No. US20030095964A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIOHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-8

Query Match 92.1%; Score 82; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 2 ISSGSGTYSDSVKG 17
61 ISSGSGTYSDSVKG 76

RESULT 6
US-10-166-626-8
Sequence 8, Application US/10166626
Publication No. US2003016876A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIOHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/166,626
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-8

Query Match 92.1%; Score 82; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 2 ISSGSGTYSDSVKG 17
61 ISSGSGTYSDSVKG 76

RESULT 7
US-10-779-461-23
Sequence 23, Application US/10779461
Publication No. US2004016654A1
GENERAL INFORMATION:
APPLICANT: MORTON, PHILIP A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
FILE REFERENCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 240
TYPE: PRT
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: phase display generated human antibody
US-10-779-461-23

Query Match 83.1%; Score 74; DB 16; Length 240;
Best Local Similarity 82.4%; Pred. No. 0.019;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DB 1 YISSGSGTYSDSVKG 17
50 YISSGSGATYADSVKG 66

RESULT 8
US-10-383-447-6
Sequence 6, Application US/10383447
Publication No. US20040096392A1
GENERAL INFORMATION:
APPLICANT: Bhaskar, Vinay
APPLICANT: de la Calle, Agustin
APPLICANT: Law, Debbie
APPLICANT: Caras, Ingrid
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Murray, Richard
APPLICANT: Afari, Daniel
TITLE OF INVENTION: Antibodies Against Cancer Antigen TWEPF2 and Uses Thereof
FILE REFERENCE: 05882.0138.NPUS00
CURRENT APPLICATION NUMBER: US/10/383,447
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/362,837
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 60/463,812
PRIOR FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial

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; FEATURE:
; OTHER INFORMATION: Heavy chain variable region
; US-10-383-447-6

Query Match
Best Local Similarity 82.0%; Score 73; DB 15; Length 120;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISSGSGTYSDSVKG 17
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Db 50 YISNGGNTYSDTVKG 66

RESULT 9
US-09-880-748-1906
; Sequence 1906, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1906
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1906

Query Match
Best Local Similarity 80.9%; Score 72; DB 10; Length 237;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISSGSGTYSDSVKG 17
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Db 50 YISSGSGTYADSVKG 66

RESULT 10
US-09-880-748-2039
; Sequence 2039, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2039
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; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-2039

Query Match
Best Local Similarity 80.9%; Score 72; DB 10; Length 237;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISSGSGTYSDSVKG 17
   ||| ||| ||| |||
Db 50 YISSGSGTYADSVKG 66

RESULT 11
US-10-293-418-1906
; Sequence 1906, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1906
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1906

Query Match
Best Local Similarity 80.9%; Score 72; DB 14; Length 237;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISSGSGTYSDSVKG 17
   ||| ||| ||| |||
Db 50 YISSGSGTYADSVKG 66

RESULT 12
US-10-293-418-2039
; Sequence 2039, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
```

```

; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2039
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-418-2039

Query Match
Best Local Similarity 80.9%; Score 72; DB 14; Length 237;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
Db 50 YISSGSGTYSDSVKG 66

RESULT 13
US-09-880-748-1905
; Sequence 1905, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1905
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1905

Query Match
Best Local Similarity 80.9%; Score 72; DB 10; Length 240;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
Db 50 YISSGSGTYSDSVKG 66

RESULT 14
US-10-293-418-1905
; Sequence 1905, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
```

```

; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1905
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-418-1905

Query Match
Best Local Similarity 80.9%; Score 72; DB 14; Length 240;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
Db 50 YISSGSGTYSDSVKG 66

RESULT 15
US-10-447-331-4
; Sequence 4, Application US/10447331
; Publication No. US2003021943A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: GEMENT,122A
; CURRENT APPLICATION NUMBER: US/10/447,331
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/515,825
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122262
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-447-331-4

Query Match
Best Local Similarity 78.7%; Score 70; DB 14; Length 121;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYSDSVKG 17
Db 51 INSGSGTYSDSVKG 66

RESULT 16
US-10-460-471-31
; Sequence 31, Application US/10460471
; Publication No. US2003020690A1
; GENERAL INFORMATION:
; APPLICANT: TERNYCK, THERESA
; APPLICANT: AVRAMEAS, ALEXANDRE
; APPLICANT: BUTTIN, GERARD
; APPLICANT: AVRAMEAS, STRAITTIS
```

```
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/10/460,471
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/09/497,997C
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-31
```

```
Query Match 77.5%; Score 69; DB 14; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.0068;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 YISGSGSTYSDSVKG 17
||| ||| ||| ||| |||
Db 1 YISRGVSTYSDTVKG 17
```

```
RESULT 17
US-10-460-471-19
; Sequence 19, Application US/10460471
; Publication No. US20030206900A1
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/10/460,471
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/09/497,997C
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-19
```

```
Query Match 77.5%; Score 69; DB 14; Length 21;
Best Local Similarity 76.5%; Pred. No. 0.0083;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 YISGSGSTYSDSVKG 17
||| ||| ||| ||| |||
Db 3 YISRGVSTYSDTVKG 19
```

```
RESULT 18
US-10-460-471-4
; Sequence 4, Application US/10460471
; Publication No. US20030206900A1
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO CI
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/10/460,471
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/09/497,997C
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-4
```

```
Query Match 77.5%; Score 69; DB 14; Length 22;
Best Local Similarity 76.5%; Pred. No. 0.0087;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 YISGSGSTYSDSVKG 17
||| ||| ||| ||| |||
Db 3 YISRGVSTYSDTVKG 19
```

```
RESULT 19
US-10-460-471-20
; Sequence 20, Application US/10460471
; Publication No. US20030206900A1
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO CI
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/10/460,471
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/09/497,997C
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-20
```

Query Match 77.5%; Score 69; DB 14; Length 22;
Best Local Similarity 76.5%; Pred. No. 0.0087;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSYSDTVKG 17
DB 3 YISRGVSTYSYSDTVKG 19

RESULT 20
US-10-460-471-7

Sequence 7, Application US/10460471
Publication No. US20030206900A1
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRATIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPERO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/10/460,471
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/09/497,997C
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-7

Query Match 77.5%; Score 69; DB 14; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.012;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSYSDTVKG 17
DB 3 YISRGVSTYSYSDTVKG 19

RESULT 21
US-10-144-549-21

Sequence 21, Application US/10144549
Publication No. US20030211590A1
GENERAL INFORMATION:
APPLICANT: Geneshuttle Biopharm, Inc.
APPLICANT: Hwu, Paul L.
TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
FILE REFERENCE: MHB 02-340
CURRENT APPLICATION NUMBER: US/10/144,549
CURRENT FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Membrane fusion sequence.
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: Synthetic membrane fusion sequence
US-10-144-549-21

Query Match 77.5%; Score 69; DB 14; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.012;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSYSDTVKG 17
DB 3 YISRGVSTYSYSDTVKG 19

RESULT 22
US-10-368-280-4

Sequence 4, Application US/10368280
Publication No. US20030219375A1
GENERAL INFORMATION:
APPLICANT: Washington University, St. Louis
APPLICANT: Plimica-Worms, David
TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL IMAGING, DIAGNOSTIC
FILE REFERENCE: 60005161-0022
CURRENT APPLICATION NUMBER: US/10/368,280
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 09/557,465
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 09/336,093
PRIOR FILING DATE: 1999-06-20
PRIOR APPLICATION NUMBER: US 60/090,087
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Peptide derivable from the heavy chain variable region of an anti
OTHER INFORMATION: -DNA monoclonal antibody
US-10-368-280-4

Query Match 77.5%; Score 69; DB 14; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.012;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSYSDTVKG 17
DB 3 YISRGVSTYSYSDTVKG 19

RESULT 23
US-10-374-035-4

Sequence 4, Application US/10374035
Publication No. US20030219378A1
GENERAL INFORMATION:
APPLICANT: Washington University, St. Louis
APPLICANT: Plimica-Worms, David
TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL IMAGING, DIAGNOSTIC
FILE REFERENCE: 09789280-0006
CURRENT APPLICATION NUMBER: US/10/374,035
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 10/368,280
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 09/557,465
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 09/336,093
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: US 60/090,087
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 30
TYPE: PRT

ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Peptide derivable from the heavy chain variable region of an anti
OTHER INFORMATION: -DNA monoclonal antibody
US-10-374-035-4

Query Match 77.5%; Score 69; DB 14; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.012;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
||| ||| ||| ||| |||
Db 3 YISRGVSTYSDTVKG 19

RESULT 24
US-10-460-471-9
Sequence 9, Application US/10460471
Publication No. US20030206900A1

GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPEETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/10/460,471
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/09/497,997C
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-9

Query Match 77.5%; Score 69; DB 14; Length 31;
Best Local Similarity 76.5%; Pred. No. 0.012;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
||| ||| ||| ||| |||
Db 4 YISRGVSTYSDTVKG 20

RESULT 25
US-10-460-471-23
Sequence 23, Application US/10460471
Publication No. US20030206900A1

GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPEETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/10/460,471

CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/09/497,997C
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 33
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-23

Query Match 77.5%; Score 69; DB 14; Length 33;
Best Local Similarity 76.5%; Pred. No. 0.013;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
||| ||| ||| ||| |||
Db 3 YISRGVSTYSDTVKG 19

RESULT 26
US-10-460-471-10
Sequence 10, Application US/10460471
Publication No. US20030206900A1
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPEETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/10/460,471
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/09/497,997C
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 49
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-10

Query Match 77.5%; Score 69; DB 14; Length 49;
Best Local Similarity 76.5%; Pred. No. 0.019;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
||| ||| ||| ||| |||
Db 22 YISRGVSTYSDTVKG 38

RESULT 27
US-10-460-471-26
Sequence 26, Application US/10460471
Publication No. US20030206900A1
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD


```

; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002905
; CURRENT APPLICATION NUMBER: US/10/275,180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
; US-10-275-180A-26

Query Match      76.4%; Score 68; DB 14; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.0093;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 ISSGSGSTYYSDSVKG 17
DB      2 ISSGSGSTYYPDSDVKG 17

RESULT 32
US-10-286-132A-26
; Sequence 26, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Lobuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002907
; CURRENT APPLICATION NUMBER: US/10/286,132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
; US-10-286-132A-26

Query Match      76.4%; Score 68; DB 14; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.0093;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 ISSGSGSTYYSDSVKG 17
DB      2 ISSGSGSTYYPDSDVKG 17

RESULT 33
US-10-477-377-9
; Sequence 9, Application US/10477377
; Publication No. US20040213788A1
; GENERAL INFORMATION:
; APPLICANT: Sweet, Raymond
; APPLICANT: Tornetta, Mark
; APPLICANT: Matlam, Trevor
; TITLE OF INVENTION: Anti-RANK Ligand Monoclonal Antibodies
```

```

; TITLE OF INVENTION: Useful in Treatment of RANK Ligand Mediated Disorders
; FILE REFERENCE: GP50050
; CURRENT APPLICATION NUMBER: US/10/477,377
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US02/14246
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/292,031
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-477-377-9

Query Match      76.4%; Score 68; DB 17; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.0093;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 ISSGSGSTYYSDSVKG 17
DB      2 ISSGSGSTYYPDSDVKG 17

RESULT 34
US-09-840-459-53
; Sequence 53, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: METHODS OF USE THEREFOR
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-840-459-53

Query Match      76.4%; Score 68; DB 9; Length 87;
Best Local Similarity 70.6%; Pred. No. 0.047;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 YISGSGSTYYSDSVKG 17
DB      39 YISNGSGSTYYPDVTKG 55

RESULT 35
US-10-766-773-53
; Sequence 53, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
```



```
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-028
CURRENT APPLICATION NUMBER: US/10/766,773
PRIOR FILING DATE: 2004-01-27
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 09/497,625
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 09/359,193
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 09/121,781
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 53
LENGTH: 87
TYPE: PRT
ORGANISM: Mus musculus
US-10-766-773-53
```

```
Query Match 76.4%; Score 68; DB 16; Length 87;
Best Local Similarity 70.6%; Pred. No. 0.047;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 YISGGSGTYSYSPVKG 17
DB 39 YISNGGSGTYPPTVKG 55
```

```
RESULT 36
US-10-766-610-53
Sequence 53, Application US/10766610
Publication No. US20040132980A1
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-029
CURRENT APPLICATION NUMBER: US/10/766,610
CURRENT FILING DATE: 2004-01-27
PRIOR FILING DATE: 09/840,459
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 53
LENGTH: 87
TYPE: PRT
ORGANISM: Mus musculus
US-10-766-610-53
```

```
Query Match 76.4%; Score 68; DB 16; Length 87;
Best Local Similarity 70.6%; Pred. No. 0.047;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 YISGGSGTYSYSPVKG 17
DB 39 YISNGGSGTYPPTVKG 55
```

```
RESULT 37
US-10-733-563-53
Sequence 53, Application US/10733563
Publication No. US20040151721A1
GENERAL INFORMATION:
APPLICANT: O'Keefe, Theresa
APPLICANT: Ponath, Paul
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 10448-213001
CURRENT APPLICATION NUMBER: US/10/733,563
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: US 10/272,899
PRIOR FILING DATE: 2002-10-17
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: US 60/392,364
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 87
TYPE: PRT
ORGANISM: Mus musculus
US-10-733-563-53
```

```
Query Match 76.4%; Score 68; DB 16; Length 87;
Best Local Similarity 70.6%; Pred. No. 0.047;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 YISGGSGTYSYSPVKG 17
DB 39 YISNGGSGTYPPTVKG 55
```

```
RESULT 38
US-09-840-459-49
Sequence 49, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 49
LENGTH: 89
TYPE: PRT
ORGANISM: Mus musculus
US-09-840-459-49
```

```
Query Match 76.4%; Score 68; DB 9; Length 89;
Best Local Similarity 87.5%; Pred. No. 0.048;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 2 ISSGSGTYYSDSVKG 17
Db 42 ISSGSGTYYPSVKG 57

RESULT 39
US-10-766-773-49
; Sequence 49, Application US/10766773
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-773-49

Query Match 76.4%; Score 68; DB 16; Length 89;
Best Local Similarity 87.5%; Pred. No. 0.048;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 42 ISSGSGTYYPSVKG 57

RESULT 40
US-10-766-610-49
; Sequence 49, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49

; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-610-49

Query Match 76.4%; Score 68; DB 16; Length 89;
Best Local Similarity 87.5%; Pred. No. 0.048;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 42 ISSGSGTYYPSVKG 57

Search completed: December 17, 2004, 18:37:58
Job time : 33.8539 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 17, 2004, 18:11:22 ; Search time 6.68539 seconds
(without alignments)
244.665 Million cell updates/sec

Title: US-10-089-500-4

Perfect score: 89

Sequence: 1 YISSGSGSTYSPDVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	83.1	111	2	PH1007
2	71	79.8	83	2	S21593
3	71	79.8	113	2	S26468
4	71	79.8	117	1	HVMS34
5	68	76.4	83	2	C25913
6	68	76.4	94	2	S14580
7	68	76.4	102	2	S14581
8	68	76.4	106	2	PH1008
9	68	76.4	108	2	S24251
10	68	76.4	108	2	PH1010
11	68	76.4	117	1	HVMS84
12	68	76.4	118	2	PH0097
13	68	76.4	119	2	F27888
14	68	76.4	120	2	S55537
15	68	76.4	120	2	S55536
16	68	76.4	122	2	E27888
17	67	75.3	108	2	PL0248
18	67	75.3	118	2	S20641
19	67	75.3	138	2	S09258
20	66	74.2	97	2	S24252
21	66	74.2	98	2	S26891
22	66	74.2	98	2	S26930
23	66	74.2	110	2	PH1652
24	66	74.2	114	2	S31120
25	66	74.2	118	2	S31105
26	66	74.2	119	2	D27889
27	66	74.2	128	2	S26790
28	66	74.2	137	2	I47193
29	65	73.0	118	2	S00700

30	65	73.0	121	2	I27887	Ig heavy chain V r
31	65	73.0	123	2	S63597	Ig heavy chain V r
32	65	73.0	124	2	C27888	Ig heavy chain V r
33	65	73.0	213	2	S68213	Ig heavy chain (Ma
34	65	73.0	548	2	S38864	Ig epsilon chain C
35	64	71.9	97	2	PH0875	Ig heavy chain V r
36	64	71.9	98	1	HVMS96	Ig heavy chain V r
37	64	71.9	101	2	C27889	Ig heavy chain V r
38	64	71.9	119	2	B27889	Ig heavy chain V r
39	64	71.9	121	2	A27888	Ig heavy chain V r
40	64	71.9	121	2	B27888	Ig heavy chain V r
41	64	71.9	152	2	B26471	Ig heavy chain pre
42	63	70.8	102	2	PH1017	Ig heavy chain V r
43	63	70.8	119	1	AIH08R	Ig heavy chain V-I
44	63	70.8	135	2	I37778	Ig variable region
45	63	70.8	140	2	I47204	Ig heavy chain var

ALIGNMENTS

RESULT 1

PH1007 Ig heavy chain V region (clone 163-cl) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PH1007

R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B ce

A/Reference number: PH0971; PMID:9281444; PMID:1512540

A/Accession: PH1007

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-111 <rtl>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; Immunoglobulin

F/15-98/Domain: Immunoglobulin homology <IMM>

Query Match 83.1%; Score 74; DB 2; Length 111;

Best Local Similarity 82.4%; Pred. No. 0.00056; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISSGSGSTYSPDVKG 17

Db 50 YISSGSGSTYSPDVKG 66

RESULT 2

S21593 Ig heavy chain V region (10C5) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C/Accession: S21593

R/Kaartinen, M.

submitted to the EMBL Data Library, May 1992

A/Reference number: S21591

A/Accession: S21593

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-83 <KAA>

A/Cross-references: EMBL:X66457; NID:G51598; PIDD:CAA47072.1; PIDD:G51599

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; Immunoglobulin

Query Match 79.8%; Score 71; DB 2; Length 83;

Best Local Similarity 76.5%; Pred. No. 0.0012; Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISSGSGSTYSPDVKG 17

Db 20 YISSGSGSTYSPDVKG 36

RESULT 3
S26468
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S26468
R/Kavaler, J.
submitted to the EMBL Data Library, April 1991
A/Reference number: S26459
A/Accession: S26468
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-113 <RAV>
A/Cross-references: EMBL:X59107; NID:G51944; PIDN:CAA41833.1; PID:G51945
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/11-94/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 71; DB 2; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.0016;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYTTPDSVKG 17
||||| ||| : |||
Db 46 YISSGSGTYTTPDSVKG 62

RESULT 4
HMS34
Ig heavy chain precursor V region (345) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C/Accession: J0502
R/Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A/Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A/Reference number: J0501; MUID:89279149; PMID:2499654
A/Accession: J0502
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-117 <LEV>
A/Cross-references: UNIPROT:P18526
A/Experimental source: strain BALB/cJ
A/Note: this sequence belongs to the VH7183 subfamily
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-19/Domain: signal sequence; #status predicted <SIG>
F/20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
F/34-117/Domain: immunoglobulin homology <IMM>
F/41-115/Disulfide bonds: #status predicted

Query Match 79.8%; Score 71; DB 1; Length 117;
Best Local Similarity 76.5%; Pred. No. 0.0017;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYTTPDSVKG 17
||||| ||| : |||
Db 69 YISSGSGTYTTPDSVKG 85

RESULT 5
C25913
Ig heavy chain V region (BFL14) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C/Accession: C25913
R/Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
A/Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
A/Reference number: A94148; MUID:8715692; PMID:3104915
A/Accession: C25913

A/Molecule type: DNA
A/Residues: 1-83 <LAW>
A/Cross-references: UNIPROT:Q920E7
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 76.4%; Score 68; DB 2; Length 83;
Best Local Similarity 87.5%; Pred. No. 0.0033;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYTTPDSVKG 17
||||| ||| ||| |||
Db 36 ISSGSGTYTTPDSVKG 51

RESULT 6
S14580
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S14580
R/Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A/Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH CI
A/Reference number: S14484
A/Accession: S14580
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-94 <CHE>
A/Cross-references: EMBL:X58652; NID:G51293; PIDN:CAA41509.1; PID:G51294
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 94;
Best Local Similarity 87.5%; Pred. No. 0.0037;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYTTPDSVKG 17
||||| ||| ||| |||
Db 43 ISSGSGTYTTPDSVKG 58

RESULT 7
S14581
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S14581
R/Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A/Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH CI
A/Reference number: S14484
A/Accession: S14581
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-102 <CHE>
A/Cross-references: EMBL:X58653; NID:G51295; PIDN:CAA41510.1; PID:G51296
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 102;
Best Local Similarity 87.5%; Pred. No. 0.004;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYTTPDSVKG 17
||||| ||| ||| |||
Db 43 ISSGSGTYTTPDSVKG 58

RESULT 8
PH1008

Ig heavy chain V region (clone 83-cl) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1008
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Matton, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1008
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-106 <TIL>
 A:Experimental source: B cell, strain [NZB x NZM]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 106;
 Best Local Similarity 70.6%; Pred. No. 0.0042;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVKG 17
 Db 50 YISGGSGTYSDSVKG 66

RESULT 9
 S24251
 Ig heavy chain V region (NS4p3-D-JH4) - human
 C:Species: Homo sapiens (man)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S24251
 R:Stewart, A.K.; Huang, C.; Scollary, B.D.; Schwartz, R.S.
 submitted to the EMBL Data Library, June 1992
 A:Description: A single VH gene predominates in the rearranged and expressed human B cell
 A:Reference number: S24247
 A:Accession: S24251
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-108 <STB>
 A:Cross-references: EMBL:X67072; NID:g38401; PIDD:CAA47457.1; PIDD:g38402
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 108;
 Best Local Similarity 76.5%; Pred. No. 0.0043;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVKG 17
 Db 46 YISGGSGTYSDSVKG 62

RESULT 10
 PH1010
 Ig heavy chain V region (clone 17a.93) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1010
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Matton, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1010
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-108 <TIL>
 A:Experimental source: B cell, strain [NZB x NZM]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 108;
 Best Local Similarity 87.5%; Pred. No. 0.0043;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YISGGSGTYSDSVKG 17
 Db 51 YISGGSGTYSDSVKG 66

RESULT 11
 HWS84
 Ig heavy chain precursor V region (5-84) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
 C:Accession: J70505
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary in
 A:Reference number: J70501; MUID:89279149; PMID:2499654
 A:Accession: J70505
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Cross-references: UNIPROT:P18525
 A:Experimental source: strain BALB/cJ
 A:Note: this sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
 F:24-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 76.4%; Score 68; DB 1; Length 117;
 Best Local Similarity 70.6%; Pred. No. 0.0046;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVKG 17
 Db 69 YISGGSGTYSDSVKG 85

RESULT 12
 PH0097
 Ig heavy chain V region (anti-cyclosporin B) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996
 C:Accession: PH0097
 R:Schmutter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Queniaux, V.F.J.; Ve
 Mol. Immunol. 27, 1029-1038, 1990
 A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
 A:Reference number: PH0087; MUID:91042649; PMID:2122240
 A:Accession: PH0097
 A:Molecule type: mRNA
 A:Residues: 1-118 <SCH>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:15-98/Domain: heterotetramer; immunoglobulin
 F:31-35/Region: complementarity-determining 1
 F:50-66/Region: complementarity-determining 2
 F:99-105/Region: complementarity-determining 3

Query Match 76.4%; Score 68; DB 2; Length 118;
 Best Local Similarity 87.5%; Pred. No. 0.0047;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YISGGSGTYSDSVKG 17
 Db 51 YISGGSGTYSDSVKG 66

RESULT 13
 F27888

Ig heavy chain V region (H158-89H4) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C/Accession: F27888
R/Caton, A.J.; Brownlee, G.G.; Staedt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response to a C/KeyWords: heterotetramer; immunoglobulin
F/15-96/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0047;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
DB 51 ISSGSGTYYPDVSKG 66

RESULT 14
S55537
Ig heavy chain V region pe21 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C/Accession: S55537
R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
utations in the variable region genes.
A/Reference number: S55528; MWID:95239763; PMID:7536850
A/Accession: S55537
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-120 <BOB>
A/Cross-references: EMBL:X82590; NID:g854306; PIDD:CAAS7926.1; PID:g854307
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/KeyWords: heterotetramer; immunoglobulin
F/14-97/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 120;
Best Local Similarity 87.5%; Pred. No. 0.0047;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
DB 50 ISSGSGTYYPDVSKG 65

RESULT 15
S55536
Ig heavy chain V region pe20 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C/Accession: S55536
R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
utations in the variable region genes.
A/Reference number: S55528; MWID:95239763; PMID:7536850
A/Accession: S55536
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-120 <BOB>
A/Cross-references: EMBL:X82589; NID:g854304; PIDD:CAAS7925.1; PID:g854305
C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/KeyWords: heterotetramer; immunoglobulin
F/14-97/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 120;
Best Local Similarity 87.5%; Pred. No. 0.0047;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
DB 50 ISSGSGTYYPDVSKG 65

RESULT 16
E27888
Ig heavy chain V region (H35-C6) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C/Accession: E27888
R/Caton, A.J.; Brownlee, G.G.; Staedt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response to a d
A/Reference number: A91043; MWID:86300658; PMID:2427335
A/Accession: E27888
A/Molecule type: DNA
A/Residues: 1-122 <CAT>
A/Experimental source: strain Balb/c
A/Note: this sequence was determined from the germline gene
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/KeyWords: heterotetramer; immunoglobulin
F/15-96/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 122;
Best Local Similarity 87.5%; Pred. No. 0.0048;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
DB 51 ISSGSGTYYPDVSKG 66

RESULT 17
P10248
Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C/Accession: P10248
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Redic, M.Z.; Pisetky, D.; Marshak-Rothstein, A
U. Exp. Med. 171, 285-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A/Reference number: P10231; MWID:90111618; PMID:2104919
A/Accession: P10248
A/Molecule type: mRNA
A/Residues: 1-108 <SHL>
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/KeyWords: heterotetramer; immunoglobulin
F/1-24/Region: framework 1
F/9-92/Domain: immunoglobulin homology <IMM>
F/25-29/Region: complementarity-determining 1
F/30-43/Region: framework 2
F/44-60/Region: complementarity-determining 2
F/61-92/Region: framework 3
F/93-99/Region: complementarity-determining 3
F/100-108/Region: framework 4

Query Match 75.3%; Score 67; DB 2; Length 108;
Best Local Similarity 81.2%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
DB 45 ISSGSGTYYPDVSKG 60

```
RESULT 18
S20641
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S20641
R/Losman, M.; Faay, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A/Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A/Reference number: S20639
A/Accession: S20641
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-118 <DOS>
A/Cross-references: EMBL:X65003; NID:G52602; PIDN:CAA46136.1; PID:G52603
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          75.3%; Score 67; DB 2; Length 118;
Best Local Similarity 81.2%; Pred. No. 0.0066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ISSGSGSTYYSDSVKG 17
Db 51 ISSGSGNTYYPDVSKG 66

RESULT 19
S09258
Ig heavy chain V region precursor - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999
C/Accession: S09258
R/Hamada, H.; Maezawa, K.; Tsuruo, T.
Nucleic Acids Res. 18, 1900, 1990
A/Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody mK4
A/Reference number: S09258; MUID:90245594; PMID:2110659
A/Accession: S09258
A/Molecule type: DNA
A/Residues: 1-138 <HAM>
A/Cross-references: EMBL:X51719; NID:G53207; PIDN:CAA36012.1; PID:G297545
C/Genetics:
A/Intons: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match          75.3%; Score 67; DB 2; Length 138;
Best Local Similarity 81.2%; Pred. No. 0.0077;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ISSGSGSTYYSDSVKG 17
Db 70 ISSGSGNTYYPDVSKG 85

RESULT 20
S24252
Ig heavy chain V region (NS4P3-D-JH6) - human
C/Species: Homo sapiens (man)
C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S24252
R/Stewart, A.K.; Huang, C.; Scollier, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A/Description: A single VH gene predominates in the rearranged and expressed human B cell
A/Reference number: S24247
A/Accession: S24252
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-97 <STEW>
A/Cross-references: EMBL:X67073; NID:G38403; PIDN:CAA47458.1; PID:G38404
```

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C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match          74.2%; Score 66; DB 2; Length 97;
Best Local Similarity 76.5%; Pred. No. 0.0076;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISSGSGTYYVSDSVKG 17
Db 27 YISSGSGTYYVSDSVKG 43

RESULT 21
S26891
Ig heavy chain V region (DP-58) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S26891
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A/Reference number: S26885; MUID:93021117; PMID:1404388
A/Accession: S26891
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <TOM>
A/Cross-references: EMBL:Z12358; NID:G32935; PIDN:CAA78228.1; PID:G32936
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          74.2%; Score 66; DB 2; Length 98;
Best Local Similarity 76.5%; Pred. No. 0.0077;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISSGSGTYYSDSVKG 17
Db 50 YISSGSGTYYVSDSVKG 66

RESULT 22
S26930
Ig heavy chain V region (DP-35) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S26930
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A/Reference number: S26885; MUID:93021117; PMID:1404388
A/Accession: S26930
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <TOM>
A/Cross-references: EMBL:Z12337; NID:G32892; PIDN:CAA78207.1; PID:G32893
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          74.2%; Score 66; DB 2; Length 98;
Best Local Similarity 76.5%; Pred. No. 0.0077;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISSGSGTYYSDSVKG 17
Db 50 YISSGSGTYYVSDSVKG 66

RESULT 23
PH1652
Ig heavy chain V region (clone 5D4) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
```

C/Accession: PH1652
R/Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germ-line encoded VH3 immunoglobulin binding to staphylococcal protein A
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1652
A/Molecule type: mRNA
A/Residues: 1-110 <HIL>
A/Experimental source: B cell
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 110;
Best Local Similarity 76.5%; Pred. No. 0.0086;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
Db 42 YISSGSGTYSDSVKG 58

RESULT 24
S31120
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31120
R/Rapaport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31120
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-114 <RAA>
A/Cross-references: EMBL:X62972
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.0089;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
Db 50 YISSGSGTYSDSVKG 66

RESULT 25
S31105
Ig heavy chain (subclass IgM) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C/Accession: S31105
R/Rapaport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31105
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-118 <RAA>
A/Cross-references: EMBL:X63081; NID:932648; PIDN:CAA44803.1; PID:932649
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 118;
Best Local Similarity 76.5%; Pred. No. 0.0092;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
Db 50 YISSGSGTYSDSVKG 66

RESULT 26
D27889
Ig heavy chain V region (H36-2) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C/Accession: D27889
R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response to a de
A/Reference number: A91043; MUID:86300658; PMID:2427335
A/Accession: D27889
A/Molecule type: DNA
A/Residues: 1-119 <CAT>
A/Experimental source: strain Balb/c
A/Note: this sequence was determined from the germ-line gene
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus he
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 119;
Best Local Similarity 81.2%; Pred. No. 0.0093;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYSDSVKG 17
Db 51 ISDGSGTYSDSVKG 66

RESULT 27
S26790
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26790
R/Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A/Reference number: S26786; MUID:92111632; PMID:1730251
A/Accession: S26790
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-128 <MOR>
A/Cross-references: EMBL:X61013; NID:932798; PIDN:CAA4347.1; PID:91335128
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 128;
Best Local Similarity 76.5%; Pred. No. 0.01;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17
Db 50 YISSGSGTYSDSVKG 66

RESULT 28
I47193
Ig heavy chain variable VDI region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47193
R/Sun, J.; Kacskovics, I.; Brown, W.R.; Butler, J.E.
J. Immunol. 153, 5618-5627, 1994
A/Title: Expressed swine VH genes belong to a small VH gene family homologous to human Vr

A:Reference number: 147177, MUID:95081609, PMID:7989761
A:Accession: 147193
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-137 <SD>
A:Cross-references: EMBL:U15452, NID:G5713390, PID:AAA67018.1, PID:G5713391
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 137;
Best Local Similarity 75.0%; Pred. No. 0.011; 2; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 70 ISSGSGTYYSDSVKG 85

RESULT 29
Ig heavy chain V region - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C:Accession: S00700
R:Yamawaki-Kataoka, Y., Honjo, T.
Nucleic Acids Res. 15, 5889, 1987
A:Title: Nucleotide sequences of variable region segments of the immunoglobulin heavy chain
A:Reference number: S00700, MUID:87289054, PMID:3112743
A:Accession: S00700
A:Molecule type: DNA
A:Residues: 1-118 <YAM>
A:Cross-references: EMBL:Y00380, NID:G64810, PID:CAA68452.1, PID:G64811
A:Note: the sequence was determined from the germine gene
C:Genetics: 15/3
A:Introns: 15/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 118;
Best Local Similarity 75.0%; Pred. No. 0.013; 3; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 70 ISSGSGTYYSDSVKG 85

RESULT 30
Ig heavy chain V region (H37-45) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: I27887
R:Catton, A.J., Brownlee, G.G., Staudt, L.M., Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043, MUID:86300658, PMID:2427335
A:Accession: I27887
A:Molecule type: DNA
A:Residues: 1-121 <CAT>
A:Experimental source: strain Balb/c
A:Note: this sequence was determined from the germine gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.013; 2; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 70 ISSGSGTYYSDSVKG 85

Db 51 ISSGSGTYYSDSVKG 66

RESULT 31
Ig heavy chain, V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S63597
R:Verdaguer, N., Mateu, M.G., Bravo, J., Domingo, E., Fita, I.
J. Mol. Biol. 256, 364-376, 1996
A:Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in a neutral
A:Reference number: S63596, MUID:96174482, PMID:8594203
A:Accession: S63597
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-123 <VER>
A:Cross-references: GB:S61215, NID:G1336823, PID:ABA36172.1, PID:G1336824
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 123;
Best Local Similarity 81.2%; Pred. No. 0.014; 2; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 51 ISSGSGTYYSDSVKG 66

RESULT 32
Ig heavy chain V region (H37-62) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: C27888
R:Catton, A.J., Brownlee, G.G., Staudt, L.M., Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043, MUID:86300658, PMID:2427335
A:Accession: C27888
A:Molecule type: DNA
A:Residues: 1-124 <CAT>
A:Experimental source: strain Balb/c
A:Note: this sequence was determined from the germine gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 124;
Best Local Similarity 81.2%; Pred. No. 0.014; 2; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 51 ISSGSGTYYSDSVKG 66

RESULT 33
Ig heavy chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Jul-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: S68213
R:Takagi, M., Kohda, K., Hamuro, T., Harada, A., Yamaguchi, H., Kamachi, M., Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211, MUID:96085223, PMID:7498516
A:Accession: S68213
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA

A;Residues: 1-213 <TK>
A;Cross-references: UNIPROT:Q91205; EMBL:D39667
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;137-201/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 213;
Best Local Similarity 70.6%; Pred. No. 0.023;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGSGGTYSPSVKG 17
||||| |||:||||
DB 50 YISGSSSTIYADTVKG 66

RESULT 34

Ig epsilon chain C region - mouse (fragment)
S38864
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C;Accession: S38864
R;KIP, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of an
A;Reference number: S38864
A;Accession: S38864
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-548 <KIP>
A;Cross-references: EMBL:Z27397; NID:G416537; PIDN:CAA81788.1; PID:G940782
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 548;
Best Local Similarity 81.2%; Pred. No. 0.059;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYSPSVKG 17
||||| |||:||||
DB 51 ISSGTYTYPDSVKG 66

RESULT 35

Ig heavy chain V region (anti-DNA, H2F) - human (fragment)
PH0875
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: PH0875
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MVID:92078875; PMID:1660528
A;Accession: PH0875
A;Molecule type: DNA
A;Residues: 1-97 <MAN>
A;Cross-references: UNIPROT:Q9UL91
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
F;30-35/Region: complementarity-determining 1
F;49-66/Region: complementarity-determining 2

Query Match 71.9%; Score 64; DB 2; Length 97;
Best Local Similarity 76.5%; Pred. No. 0.015;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGSGGTYSPSVKG 17
||||| |||:||||
DB 49 YISSRGSSTIYADSVKG 65

RESULT 36

HVMS96

Ig heavy chain V region (6.96) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: J70501
R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary in
A;Reference number: J70501; MVID:89279149; PMID:249654
A;Accession: J70501
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-98 <LEV>

Query Match 71.9%; Score 64; DB 1; Length 98;
Best Local Similarity 81.2%; Pred. No. 0.015;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGSGGTYSPSVKG 17
||||| |||:||||
DB 51 ISDGSGTYTYPDSVKG 66

RESULT 37

Ig heavy chain V region (H220-25) - mouse
C27889
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: C27889
R;Caton, A.J.; Brownlee, G.G.; Straud, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a de
A;Reference number: A91043; MVID:86300658; PMID:2427335
A;Accession: C27889
A;Molecule type: DNA
A;Residues: 1-101 <CAT>
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus he
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 71.9%; Score 64; DB 2; Length 101;
Best Local Similarity 81.2%; Pred. No. 0.016;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGSGGTYSPSVKG 17
||||| |||:||||
DB 33 ISDGSGTYTYPDSVKG 48

RESULT 38

Ig heavy chain V region (H146-24B3) - mouse
B27889
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: B27889
R;Caton, A.J.; Brownlee, G.G.; Straud, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a de
A;Reference number: A91043; MVID:86300658; PMID:2427335
A;Accession: B27889
A;Molecule type: DNA
A;Residues: 1-119 <CAT>

A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus he

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 64; DB 2; Length 119;
Best Local Similarity 81.2%; Pred. No. 0.018;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGSGTYTYSDSVKG 17
||| ||| ||| ||| |||
DB 51 ISSGSGTYTYPDSVKG 66

RESULT 39

A27888

Ig heavy chain V region (H37-84) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: A27888

R:Caton, A.U.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a d

A:Reference number: A91043; MID:86300658; PMID:2427335

A:Accession: A27888

A:Molecule type: DNA

A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 64; DB 2; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.019;

QY 2 ISSGSGTYTYSDSVKG 17
||| ||| ||| ||| |||
DB 51 ISSGSGTYTYPDSVKG 66

RESULT 40

B27888

Ig heavy chain V region (H37-311) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: B27888

R:Caton, A.U.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a d

A:Reference number: A91043; MID:86300658; PMID:2427335

A:Accession: B27888

A:Molecule type: DNA

A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 64; DB 2; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.019;

QY 2 ISSGSGTYTYSDSVKG 17
||| ||| ||| ||| |||
DB 51 ISSGSGTYTYPDSVKG 66

Search completed: December 17, 2004, 18:30:14
Job time : 7.68539 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:29:23 ; Search time 50.809 Seconds
(without alignments)
192.513 Million cell updates/sec

Title: US-10-089-500-4

Sequence: 1 YISSGGSGSTYSDSVK 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	79.8	117	1 HV55 MOUSE	P18526 mus musculus
2	71	79.8	127	2 BAD00209	Bad00209 camelus d
3	70	78.7	127	2 BAD00303	Bad00303 camelus d
4	68	76.4	117	1 HV54 MOUSE	P18525 mus musculus
5	68	76.4	119	2 Q920E7	Q920E7 mus musculus
6	67	75.3	116	2 BAD00431	Bad00431 camelus d
7	66	74.2	117	2 AAL35877	AAL35877 lama glam
8	66	74.2	120	2 BAD00231	Bad00231 camelus d
9	66	74.2	122	2 BAD00455	Bad00455 camelus d
10	66	74.2	124	2 BAD00233	Bad00233 camelus d
11	66	74.2	126	2 BAD00225	Bad00225 camelus d
12	66	74.2	126	2 BAD00420	Bad00420 camelus d
13	66	74.2	128	2 BAD00406	Bad00406 camelus d
14	66	74.2	128	2 BAD00444	Bad00444 camelus d
15	66	74.2	129	2 BAD00668	Bad00668 camelus d
16	66	74.2	131	2 BAD00494	Bad00494 camelus d
17	65	73.0	126	2 BAD00210	Bad00210 camelus d
18	65	73.0	255	2 Q6KB05	Q6KB05 mus musculus
19	65	73.0	255	2 CAG34081	CAG34081 mus musculus
20	64	71.9	98	1 HV57 MOUSE	P18528 mus musculus
21	64	71.9	120	2 BAD00519	Bad00519 camelus d
22	64	71.9	123	2 BAD00417	Bad00417 camelus d
23	64	71.9	125	2 BAD00474	Bad00474 camelus d
24	64	71.9	128	2 BAD00403	Bad00403 camelus d
25	64	71.9	131	2 BAD00240	Bad00240 camelus d
26	63	70.8	119	1 HV3L HUMAN	P01773 homo sapien
27	63	70.8	119	2 BAD00492	Bad00492 camelus d
28	63	70.8	125	2 BAD00491	Bad00491 camelus d
29	63	70.8	126	2 BAD00480	Bad00480 camelus d
30	63	70.8	126	2 BAD00510	Bad00510 camelus d
31	63	70.8	127	2 BAD00602	Bad00602 camelus d

32	63	70.8	130	2 BAD00691	Bad00691 camelus d
33	62	69.7	117	1 HV58 MOUSE	P18529 mus musculus
34	62	69.7	118	2 AAL35871	AAL35871 lama glam
35	62	69.7	123	2 BAD00234	Bad00234 camelus d
36	62	69.7	124	2 BAD00388	Bad00388 camelus d
37	62	69.7	136	2 BAD00606	Bad00606 camelus d
38	62	69.7	614	2 Q6DDQ7	Q6DDQ7 xenopus lae
39	61	68.5	117	2 AAL35869	AAL35869 lama glam
40	61	68.5	119	2 BAD00422	Bad00422 camelus d
41	61	68.5	121	2 BAD00273	Bad00273 camelus d
42	61	68.5	121	2 BAD00402	Bad00402 camelus d
43	61	68.5	121	2 BAD00413	Bad00413 camelus d
44	61	68.5	121	2 BAD00459	Bad00459 camelus d
45	61	68.5	123	2 BAD00582	Bad00582 camelus d

ALIGNMENTS

RESULT 1			
HV55_MOUSE	STANDARD;	PRT;	117 AA.
ID HV55_MOUSE			
AC P18526;			
DT 01-NOV-1990 (Rel. 16, Created)			
DT 01-NOV-1990 (Rel. 16, Last sequence update)			
DT 15-JUL-1999 (Rel. 38, Last annotation update)			
DE Ig heavy chain V region 345 precursor.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxId=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=BALB/CJ;			
RX MEDLINE=89279149; PubMed=2499654;			
RA Levy N.S., Malipiero U.V., Lebecqz S.G., Gearhart P.J.;			
RT "Early onset of somatic mutation in immunoglobulin VH genes during the			
RT primary immune response.";			
RL J. Exp. Med. 169:2007-2019(1989).			
CC -I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.			
DR PIR; UT0502; HYMS34.			
DR HSSP; P01783; IIGC.			
DR InterPro; IPR007110; Ig_1like.			
DR InterPro; IPR003596; Ig_V.			
DR Pfam; PF00047; Ig_1.			
DR SMART; SM00406; IGV_1.			
DR PROSITE; PS50835; IG_LIKE; 1.			
KW Immunoglobulin V region; Signal.			
FT SIGNAL 1 19			
FT CHAIN 20 117			
FT DOMAIN 20 49			
FT DOMAIN 50 54			
FT DOMAIN 55 68			
FT DOMAIN 69 85			
FT DOMAIN 86 117			
FT DISULFID 41 115			
FT NON TER 117 117			
SO SEQUENCE 117 AA; 12902 MW; 4938084627ACA99A CRC64;			
Query Match	79.8%;	Score 71;	DB 1; Length 117;
Best Local Similarity	76.5%;	Pred. No. 0.0031;	
Matches 13; Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;
OY 1 YISSGGSGTYYSDSVK 17			
Db 69 YISSGGSGTYYPDYVK 85			
RESULT 2			
BAD00209	PRELIMINARY;	PRT;	127 AA.
AC BAD00209;			
DT 02-MAR-2004 (TrEMBLrel. 27, Created)			

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DT 02-MAR-2004 (T-EMBLrel. 27, last sequence update)
DE 02-MAR-2004 (T-EMBLrel. 27, last annotation update)
GN Immunoglobulin heavy chain VHD region (Fragment).
GN IGVR.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091847; BAD00209.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 127 AA; 13172 MW; 997A29430D12FA9F CRC64;

Query Match 79.8%; Score 71; DB 2; Length 127;
Best Local Similarity 81.2%; Pred. No. 0.0034;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGCTTYSDSVKG 17
DB 51 ISPGCTGTYYADSVKG 66

RESULT 3
BAD00303 PRELIMINARY; PRT; 127 AA.
AC BAD00303;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, last sequence update)
DE 02-MAR-2004 (T-EMBLrel. 27, last annotation update)
DE Immunoglobulin heavy chain VHD region (Fragment).
GN IGVR.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091941; BAD00303.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 127 AA; 13452 MW; FCB3C0201720A482 CRC64;

Query Match 78.7%; Score 70; DB 2; Length 127;
Best Local Similarity 81.2%; Pred. No. 0.0049;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGCTTYSDSVKG 17
DB 51 ISSGSGASTYTDVKG 66

RESULT 4
HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response."
RL J. Exp. Med. 169:2007-2019 (1989).
CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
DR PIR: J70505; HVMS84.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 Ig heavy chain V region 5-84.
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 76.4%; Score 68; DB 1; Length 117;
Best Local Similarity 70.6%; Pred. No. 0.0094;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGCTTYSDSVKG 17
DB 69 YISSGSGCTTYPDVKG 85

RESULT 5
0920E7 PRELIMINARY; PRT; 119 AA.
ID 0920E7;
AC 0920E7;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horatis O., Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1; -.
DR PIR; C25913; C25913.
DR HSSP; P01783; 1IGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 119 AA; 13025 MW; F6B90404381CA7C CRC64;

Query Match 76.4%; Score 68; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.0095;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 ISSGSGCTTYSDSVKG 17
```

Db 51 ISSGSGSTYYADSVKG 66

RESULT 6

ID BAD00431 PRELIMINARY; PRT; 116 AA.

AC BAD00431;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.,
RT "libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092069; BAD00431.1; -.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12524 MW; F9C289C9D17B7C58 CRC64;

Query Match

Best Local Similarity 75.3%; Score 67; DB 2; Length 116;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ISSGSGSTYYADSVKG 17
Db 51 ISSGSGSTYYADSVKG 66

RESULT 7

ID AAL35877 PRELIMINARY; PRT; 117 AA.

AC AAL35877;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Immunoglobulin heavy chain variable domain (Fragment).
OS Lama glama (Llama).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=2207448; PubMed=12009207;
RA Tania U., Dubuc G., Hirama T., Narang S.A., Mackenzie C.R.,
RT "Selection by phage display of llama conventional V(H) fragments with
heavy chain antibody V(H)H properties.";
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL; AF442946; AAL35877.1; -.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12459 MW; 08F5E4BA402F98D1 CRC64;

Query Match

Best Local Similarity 74.2%; Score 66; DB 2; Length 117;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ISSGSGSTYYADSVKG 17
Db 51 ISSGSGSTYYADSVKG 66

RESULT 8

BAD00231

ID BAD00231 PRELIMINARY; PRT; 120 AA.

AC BAD00231;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.,
RT "libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091869; BAD00231.1; -.
FT NON_TER 1 1
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 12888 MW; B5CFD3D14DA23813 CRC64;

Query Match

Best Local Similarity 74.2%; Score 66; DB 2; Length 120;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ISSGSGSTYYADSVKG 17
Db 51 ISSGSGSTYYADSVKG 66

RESULT 9

ID BAD00455 PRELIMINARY; PRT; 122 AA.

AC BAD00455;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.,
RT "libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092093; BAD00455.1; -.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13140 MW; F89DDF2022218EC5 CRC64;

Query Match

Best Local Similarity 74.2%; Score 66; DB 2; Length 122;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ISSGSGSTYYADSVKG 17
Db 51 ISSGSGSTYYADSVKG 66

RESULT 10

ID BAD00233 PRELIMINARY; PRT; 124 AA.

AC BAD00233;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.,
RT "libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092093; BAD00455.1; -.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13140 MW; F89DDF2022218EC5 CRC64;

```
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091871; BAD00233.1; -.
FT NON TER 1 1
FT NON TER 124 124
SQ SEQUENCE 124 AA; 13374 MW; FE75B41506CABD25 CRC64;

Query Match 74.2%; Score 66; DB 2; Length 124;
Best Local Similarity 75.0%; Pred. No. 0.021;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
DB 51 INSGSGTYYADSVKG 66

RESULT 11
BAD00225 PRELIMINARY; PRT; 126 AA.
AC BAD00225;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091863; BAD00225.1; -.
FT NON TER 1 1
FT NON TER 126 126
SQ SEQUENCE 126 AA; 13717 MW; 486BD741474EP26 CRC64;

Query Match 74.2%; Score 66; DB 2; Length 126;
Best Local Similarity 75.0%; Pred. No. 0.021;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
DB 51 INSGSGTYYADSVKG 66

RESULT 12
BAD00420 PRELIMINARY; PRT; 126 AA.
AC BAD00420;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
```

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OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092058; BAD00420.1; -.
FT NON TER 1 1
FT NON TER 126 126
SQ SEQUENCE 126 AA; 13569 MW; A8F3B29B6C9BE29D CRC64;

Query Match 74.2%; Score 66; DB 2; Length 126;
Best Local Similarity 75.0%; Pred. No. 0.021;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
DB 51 INSGSGTYYADSVKG 66

RESULT 13
BAD00406 PRELIMINARY; PRT; 128 AA.
AC BAD00406;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092044; BAD00406.1; -.
FT NON TER 1 1
FT NON TER 128 128
SQ SEQUENCE 128 AA; 13856 MW; 7C23CF09C38B8B9A CRC64;

Query Match 74.2%; Score 66; DB 2; Length 128;
Best Local Similarity 75.0%; Pred. No. 0.021;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
DB 51 INSGSGTYYADSVKG 66

RESULT 14
BAD00444 PRELIMINARY; PRT; 128 AA.
AC BAD00444;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
```


RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB092082; BAD0044.1; -.
FT NON_TER 1 1
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 13775 MW; 85E9EDD39D9159F3 CRC64;

Query Match 74.2%; Score 66; DB 2; Length 128;
Best Local Similarity 75.0%; Pred. No. 0.021;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGSTYYSDSVKG 17
DB 51 INSGGSGSTYYADSVKG 66

RESULT 15

BAD00668 PRELIMINARY; PRT; 129 AA.

AC BAD00668;

DT 02-MAR-2004 (TEMBLrel. 27, Created)

DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)

DE Immunoglobulin heavy chain VHDJ region (Fragment).

GN IGvH.

OS Camelus dromedarius (Dromedary) (Arabian camel).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.

NCBI_TaxID=9838;

OK NCB1

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Honda T., Akahori Y., Kurosawa Y.;

RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and

RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB092306; BAD00668.1; -.

FT NON_TER 1 1

FT NON_TER 129 129

SQ SEQUENCE 129 AA; 13634 MW; 349FE94B0882DB9A CRC64;

Query Match 74.2%; Score 66; DB 2; Length 129;
Best Local Similarity 75.0%; Pred. No. 0.022;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGSTYYSDSVKG 17
DB 51 INSGGSGSTYYADSVKG 66

RESULT 16

BAD00494 PRELIMINARY; PRT; 131 AA.

AC BAD00494;

DT 02-MAR-2004 (TEMBLrel. 27, Created)

DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)

DE Immunoglobulin heavy chain VHDJ region (Fragment).

GN IGvH.

OS Camelus dromedarius (Dromedary) (Arabian camel).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.

NCBI_TaxID=9838;

OK NCB1

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Honda T., Akahori Y., Kurosawa Y.;

RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and

RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB092313; BAD00494.1; -.

FT NON_TER 1 1

FT NON_TER 131 131
SQ SEQUENCE 131 AA; 13845 MW; 22B3899E26859AD8 CRC64;

Query Match 74.2%; Score 66; DB 2; Length 131;
Best Local Similarity 75.0%; Pred. No. 0.022;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGSTYYSDSVKG 17
DB 51 INSGGSGSTYYADSVKG 66

RESULT 17

BAD00210 PRELIMINARY; PRT; 126 AA.

AC BAD00210;

DT 02-MAR-2004 (TEMBLrel. 27, Created)

DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)

DE Immunoglobulin heavy chain VHDJ region (Fragment).

GN IGvH.

OS Camelus dromedarius (Dromedary) (Arabian camel).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.

NCBI_TaxID=9838;

OK NCB1

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Honda T., Akahori Y., Kurosawa Y.;

RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and

RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB091848; BAD00210.1; -.

FT NON_TER 1 1

FT NON_TER 126 126

SQ SEQUENCE 126 AA; 13476 MW; CC4660B57AD474A1 CRC64;

Query Match 73.0%; Score 65; DB 2; Length 126;
Best Local Similarity 81.2%; Pred. No. 0.03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGSTYYSDSVKG 17
DB 51 INSGGSGSTYYADSVKG 66

RESULT 18

Q6KB05 PRELIMINARY; PRT; 255 AA.

AC Q6KB05;

DT 05-JUL-2004 (TEMBLrel. 27, Created)

DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)

DE SCFV B8E5 protein (Fragment).

GN Name=scFV B8E5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

OK NCB1

RP SEQUENCE FROM N.A.

RC STRAIN=Balb/C;

RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,

RI Brand J.P., Hoebeke J.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ746180; CAG34081.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG_1like.

DR Pfam; PF00047; IG_2.

DR SMART; SM00409; IG_2.

DR SMART; SM00406; IGv_2.

DR PROSITE; PS50835; IG_LIKE; 2.

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FT  NON_TER      1      1
SQ  SEQUENCE      255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match
Best Local Similarity 73.0%; Score 65; DB 2; Length 255;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  2 ISSGSGGTYTYPDSVKG 17
    |::|||::|||
    51 ITSGSGTYTYPDSVKG 66

RESULT 19
CAG34081 PRELIMINARY; PRT; 255 AA.
AC  CAG34081;
DT  01-JUN-2004 (TEMBLrel. 27, Created)
DT  01-JUN-2004 (TEMBLrel. 27, Last sequence update)
DE  SCFV B8B5 protein (Fragment).
GN  SCFV B8B5.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxId=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Dalb/c;
RA  Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RT  "Modulation of the M2 muscarinic receptor activity with monoclonal
RL  anti-M2 receptor antibody fragments."
RT  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AJ746180; CAG34081.1; -.
FT  NON_TER      1      1
SQ  SEQUENCE      255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match
Best Local Similarity 73.0%; Score 65; DB 2; Length 255;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  2 ISSGSGGTYTYPDSVKG 17
    |::|||::|||
    51 ITSGSGTYTYPDSVKG 66

Db  51 ITSGSGTYTYPDSVKG 66

RESULT 20
HV57_MOUSE STANDARD; PRT; 98 AA.
ID  HV57_MOUSE
AC  P18528;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig heavy chain V region 6.96.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxId=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/c;
RA  MEDLINE=89279149; PubMed=2499654;
RX  Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT  "Early onset of somatic mutation in immunoglobulin VH genes during the
RT  primary immune response."
RL  J. Exp. Med. 169:2007-2019(1989).
CC  -1- MISCELLANEOUS: This sequence belongs to the VH7.183 subfamily.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR  HSSP; P01783; 1IGC.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.

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DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS00835; IG_LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN      1      98
FT  NON_TER      98      98
SQ  SEQUENCE      98 AA; 11007 MW; B6644F7F92FBF95B CRC64;

Query Match
Best Local Similarity 71.9%; Score 64; DB 1; Length 98;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 ISSGSGGTYTYPDSVKG 17
    |::|||::|||
    51 IDSGSGTYTYPDSVKG 66

Db  51 IDSGSGTYTYPDSVKG 66

RESULT 21
BAD00519 PRELIMINARY; PRT; 120 AA.
ID  BAD00519
AC  BAD00519;
DT  02-MAR-2004 (TEMBLrel. 27, Created)
DT  02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT  02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE  Immunoglobulin heavy chain VHDJ region (Fragment).
GN  IGVH.
OS  Camelus dromedarius (Dromedary) (Arabian camel).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX  NCBI_TaxId=9838;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Spleen;
RA  Honda T., Akahori Y., Kurosawa Y.;
RT  "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT  gamma3 in vivo repertoires."
RL  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB092157; BAD00519.1; -.
FT  NON_TER      1      1
FT  NON_TER      120     120
SQ  SEQUENCE      120 AA; 13036 MW; F0A71A1C4CD0F427 CRC64;

Query Match
Best Local Similarity 71.9%; Score 64; DB 2; Length 120;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  2 ISSGSGGTYTYPDSVKG 17
    |::|||::|||
    51 IDSGSGTYTYPDSVKG 66

Db  51 IDSGSGTYTYPDSVKG 66

RESULT 22
BAD00417 PRELIMINARY; PRT; 123 AA.
ID  BAD00417
AC  BAD00417;
DT  02-MAR-2004 (TEMBLrel. 27, Created)
DT  02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT  02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE  Immunoglobulin heavy chain VHDJ region (Fragment).
GN  IGVH.
OS  Camelus dromedarius (Dromedary) (Arabian camel).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX  NCBI_TaxId=9838;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Spleen;
RA  Honda T., Akahori Y., Kurosawa Y.;
RT  "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT  gamma3 in vivo repertoires."
RL  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB092055; BAD00417.1; -.
FT  NON_TER      1      1
FT  NON_TER      123     123

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SO. SEQUENCE 123 AA; 13316 MW; 84CB9BA9C10BC846 CRC64;

Query Match 71.9%; Score 64; DB 2; Length 123;
Best Local Similarity 75.0%; Pred. No. 0.042;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 ISSGSGTYYSDSVKG 17
DB 51 ISSGSGTYYSDSVKG 66

RESULT 23

BAD00474 PRELIMINARY; PRT; 125 AA.

AC BAD00474; (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.

OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxId=9838;

RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and gamma3 in vivo repertoire.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092112; BAD00474.1; -.

FT NON_TER 1 1
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13496 MW; 65B6C5D18114730D CRC64;

Query Match 71.9%; Score 64; DB 2; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.043;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ISSGSGTYYSDSVKG 17
DB 51 VSSGSGTYYSDSVKG 66

RESULT 24

BAD00403 PRELIMINARY; PRT; 128 AA.

AC BAD00403; (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.

OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxId=9838;

RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and gamma3 in vivo repertoire.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092041; BAD00403.1; -.

FT NON_TER 1 1
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 13716 MW; 69AB271259B0A2BF CRC64;

Query Match 71.9%; Score 64; DB 2; Length 128;
Best Local Similarity 75.0%; Pred. No. 0.044;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ISSGSGTYYSDSVKG 17
DB 51 ISSGSGTYYSDSVKG 66

RESULT 25

BAD00240 PRELIMINARY; PRT; 131 AA.

AC BAD00240; (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.

OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxId=9838;

RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and gamma3 in vivo repertoire.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091878; BAD00240.1; -.

FT NON_TER 1 1
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14186 MW; D09D242CA8D06BBD CRC64;

Query Match 71.9%; Score 64; DB 2; Length 131;
Best Local Similarity 75.0%; Pred. No. 0.045;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ISSGSGTYYSDSVKG 17
DB 51 ISSGSGTYYSDSVKG 66

RESULT 26

HV3L_HUMAN STANDARD; PRT; 119 AA.

AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region BUR.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxId=9606;

RN (1)
RP SEQUENCE (MYELOMA PROTEIN BUR).
RA MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal IgA1 protease, digestion, Fab and Fc fragments, and the complete amino acid sequence of the alpha 1 heavy chain.";
RT J. Biol. Chem. 254:2865-2874 (1979).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP; P01772; 2F84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin V region; Pyrolytic carboxylic acid.

FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyroglutamate carboxylic acid.
FT DISULFID 22 96 N-linked (GLCNAC. . .).
FT CARBOHYD 28 28
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 70.8%; Score 63; DB 1; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.059;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 51 ISYGSBITYADSVKG 66

RESULT 27
BAD00492 PRELIMINARY; PRT; 119 AA.
ID BAD00492; PRELIMINARY; PRT; 119 AA.
AC BAD00492; PRELIMINARY; PRT; 119 AA.
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092130; BAD00492.1; -.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12733 MW; 106C2BF6EC1E7C14 CRC64;

Query Match 70.8%; Score 63; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.059;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 51 IISGSDNTYYADSVKG 66

RESULT 28
BAD00491 PRELIMINARY; PRT; 125 AA.
ID BAD00491; PRELIMINARY; PRT; 125 AA.
AC BAD00491; PRELIMINARY; PRT; 125 AA.
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092129; BAD00491.1; -.
FT NON_TER 1 1
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13665 MW; 13658DFBFB8F6E CRC64;

SQ SEQUENCE 125 AA; 13593 MW; F1637892B028E48C CRC64;

Query Match 70.8%; Score 63; DB 2; Length 125;
Best Local Similarity 68.8%; Pred. No. 0.062;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 51 INSGGRTYYTSVKG 66

RESULT 29
BAD00480 PRELIMINARY; PRT; 126 AA.
ID BAD00480; PRELIMINARY; PRT; 126 AA.
AC BAD00480; PRELIMINARY; PRT; 126 AA.
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092118; BAD00480.1; -.
FT NON_TER 1 1
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13500 MW; 074EB0BD13DA9531 CRC64;

Query Match 70.8%; Score 63; DB 2; Length 126;
Best Local Similarity 68.8%; Pred. No. 0.063;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKG 17
Db 51 VNSGSSRTFYADSVKG 66

RESULT 30
BAD00510 PRELIMINARY; PRT; 126 AA.
ID BAD00510; PRELIMINARY; PRT; 126 AA.
AC BAD00510; PRELIMINARY; PRT; 126 AA.
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092148; BAD00510.1; -.
FT NON_TER 1 1
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13665 MW; A8358DFBFB8F6E CRC64;

Query Match 70.8%; Score 63; DB 2; Length 126;
Best Local Similarity 75.0%; Pred. No. 0.063;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGSGGTYSDSVKG 17
 DB 51 ISSGSGDSTYVADSVKG 66

RESULT 31

ID BAD00602 PRELIMINARY; PRT; 127 AA.

AC BAD00602;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Immunoglobulin heavy chain VHDJ region (Fragment).
 GN IGVA.

OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;
 RA Honda T., Akahori Y., Kurosawa Y.;

RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
 RT gamma3 in vivo repertoire.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB092240; BAD00602.1; -

DR NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 127 AA; 13560 MW; 9E93C834DEF7C119 CRC64;

Query Match

Best Local Similarity 70.8%; Score 63; DB 2; Length 127;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGSGGTYSDSVKG 17
 DB 52 IVSGGSDSTYVADSVKG 67

RESULT 32

ID BAD00691 PRELIMINARY; PRT; 130 AA.

AC BAD00691;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Immunoglobulin heavy chain VHDJ region (Fragment).
 GN IGVA.

OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;
 RA Honda T., Akahori Y., Kurosawa Y.;

RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
 RT gamma3 in vivo repertoire.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB092329; BAD00691.1; -

DR NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 130 AA; 14108 MW; AF39A4AB9A8A8645 CRC64;

Query Match

Best Local Similarity 70.8%; Score 63; DB 2; Length 130;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGGTYSDSVKG 17
 DB 51 IVSGGSDSTYVADSVKG 66

RESULT 33
 HV58 MOUSE STANDARD; PRT; 117 AA.

AC P18529;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig heavy chain V region 5-76 precursor.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BA1B/cj;
 RX MEDLINE=89279149; PubMed=249654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during the
 RT primary immune response.";
 RL J. Exp. Med. 169:2007-2019 (1989).
 CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.

DR PIR; J0506; HYMS57.
 DR PDB; 118I; X-ray; B=20-117.
 DR PDB; 118K; X-ray; B=20-117.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IG_V_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR 3D-structure; Immunoglobulin V region, Signal.

FT SIGNAL 1 19 Ig heavy chain V region 5-76.
 FT CHAIN 20 117 Framework-1.
 FT DOMAIN 20 49 Complementarity-determining-1.
 FT DOMAIN 50 54 Framework-2.
 FT DOMAIN 55 68 Complementarity-determining-2.
 FT DOMAIN 69 85 Framework-3.
 FT DOMAIN 86 117 Framework-3.
 FT DISULFID 41 115 By similarity.
 FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;
 Query Match
 Best Local Similarity 69.7%; Score 62; DB 1; Length 117;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGSGGTYSDSVKG 17
 DB 70 ISSGGLTYTPDSVKG 85

RESULT 34

ID AAL35871 PRELIMINARY; PRT; 118 AA.

AC AAL35871;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Immunoglobulin heavy chain variable domain (Fragment).
 OS Lama glama (Llama).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OX NCBI_TaxID=9844;
 RN [1]
 RP SEQUENCE FROM N.A.

RC MEDLINE=22007448; PubMed=12009207;
 RA Tanha J., Dubuc G., Hirama T., Narang S.A., Mackenzie C.R.;

RT "Selection by phage display of llama conventional V(H) fragments with
 RT heavy chain antibody V(H)H properties.";
 RL J. Immunol. Methods 263:97-109 (2002).

DR EMBL; AF442940; AAL35871.1; -
 DR NON_TER 1
 FT NON_TER 118 118

SQ SEQUENCE 118 AA; 12594 MW; CBA02A7073EFB8B2 CRC64;
Query Match 69.7%; Score 62; DB 2; Length 118;
Best Local Similarity 68.8%; Pred. No. 0.084;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 ISSGSGCTYYSDSVKG 17
DB 51 INTSGRGTYADSVKG 66
RESULT 35
BAD00234 PRELIMINARY; PRT; 123 AA.
AC BAD00234;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, last annotation update)
DE Immunoglobulin heavy chain VHJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091872; BAD00234.1; -.
FT NON TER 1 123
SQ SEQUENCE 123 AA; 13333 MW; 9BEPD170BC27D18F CRC64;
Query Match 69.7%; Score 62; DB 2; Length 123;
Best Local Similarity 64.7%; Pred. No. 0.088;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 YISSGSGCTYYSDSVKG 17
DB 50 HISNGSGTYADSVKG 66
RESULT 36
BAD00388 PRELIMINARY; PRT; 124 AA.
AC BAD00388;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, last annotation update)
DE Immunoglobulin heavy chain VHJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092026; BAD00388.1; -.
FT NON TER 1 124
SQ SEQUENCE 124 AA; 13593 MW; F7DBFF7671BA0A0C CRC64;
Query Match 69.7%; Score 62; DB 2; Length 124;
Best Local Similarity 75.0%; Pred. No. 0.089;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGCTYYSDSVKG 17
DB 48 ISTGRLRTYYADSVKG 63
RESULT 37
BAD00606 PRELIMINARY; PRT; 136 AA.
AC BAD00606;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, last annotation update)
DE Immunoglobulin heavy chain VHJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "libraries of heavy-chain antibodies reflecting camel gamma2 and
gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092244; BAD00606.1; -.
FT NON TER 1 136
SQ SEQUENCE 136 AA; 14332 MW; B5DCA85A15DC0546 CRC64;
Query Match 69.7%; Score 62; DB 2; Length 136;
Best Local Similarity 68.8%; Pred. No. 0.098;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 ISSGSGCTYYSDSVKG 17
DB 52 INSGSDSTYYADSVKG 67
RESULT 38
Q6DD07 PRELIMINARY; PRT; 614 AA.
AC Q6DD07;
DT 01-OCT-2004 (T-EMBLrel. 28, Created)
DT 01-OCT-2004 (T-EMBLrel. 28, last sequence update)
DT 01-OCT-2004 (T-EMBLrel. 28, last annotation update)
DE Hypoetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RT "genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Maruska K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maria M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Klein S., Strausberg R.,
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC074777; AAH77477.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 614 AA; 68253 MW; 2631B7CF955270C0 CRC64;

Query Match 69.7%; Score 62; DB 2; Length 614;
 Best Local Similarity 75.0%; Pred. No. 0.48;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 ISSGSGTYYSDSVKG 17
 DB 68 ISSDGSSTYYADSVKG 83

RESULT 39

AAL35869 PRELIMINARY; PRT; 117 AA.

AC AAL35869; 02-MAR-2004 (T-EMBLrel). 27, Created)
 DT 02-MAR-2004 (T-EMBLrel). 27, Last sequence update)
 DT 02-MAR-2004 (T-EMBLrel). 27, Last annotation update)
 DE Immunoglobulin heavy chain variable domain (Fragment).
 OS Lama glama (Llama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22007448; PubMed=12009207;
 RA Tanha U., Dubuc G., Hirama T., Narang S.A., Mackenzie C.R.,
 RT "Selection by phage display of llama conventional V(H) fragments with
 RT heavy chain antibody V(H)H properties.";
 RL J. Immunol. Methods 263:97-109(2002).
 DR EMBL; AF442938; AAL35869.1; -.
 FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 12455 MW; 03CFA04B12B941B5 CRC64;

Query Match 68.5%; Score 61; DB 2; Length 117;
 Best Local Similarity 75.0%; Pred. No. 0.12;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 ISSGSGTYYSDSVKG 17
 DB 51 ISSDGSSTYYADSVKG 66

RESULT 40

BAD00422 PRELIMINARY; PRT; 119 AA.

AC BAD00422; 02-MAR-2004 (T-EMBLrel). 27, Created)
 DT 02-MAR-2004 (T-EMBLrel). 27, Last sequence update)
 DT 02-MAR-2004 (T-EMBLrel). 27, Last annotation update)
 DE Immunoglobulin heavy chain VHD region (Fragment).
 GN IGVH.

OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Honda T., Akahori Y., Kurosawa Y.,
 RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
 RT gamma3 in vivo repertoires.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB092060; BAD00422.1; -.

FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 12748 MW; 3B382D11247DFD85 CRC64;

Query Match 68.5%; Score 61; DB 2; Length 119;
 Best Local Similarity 91.7%; Pred. No. 0.12;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 GSCTYYSDSVKG 17
 DB 57 GSCTYYADSVKG 68

Search completed: December 17, 2004, 19:14:37
 Job time : 51.809 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:10:02 ; Search time 30.3933 seconds
(without alignments)
118.029 Million cell updates/sec

Title: US-10-089-500-5
Perfect score: 54
Sequence: 1 VKLGYFDS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_23sep04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003s:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	4 AAB81981	Aab81981 Gangliosid
2	54	100.0	10	6 ABU11006	Abu11006 Modified
3	54	100.0	119	4 AAB81985	Aab81985 Gangliosid
4	54	100.0	119	4 AAB81989	Aab81989 Gangliosid
5	54	100.0	119	6 ABU11012	Abu11012 Modified
6	54	100.0	119	6 ABU11010	Abu11010 Modified
7	54	100.0	130	2 AAR33256	Aar33256 Rat Immun
8	54	100.0	130	2 AAR53341	Aar53341 K6641 L c
9	54	100.0	130	2 AAY28369	Aay28369 PKM641 HA
10	54	100.0	130	3 AAB01627	Aab01627 Murine Im
11	54	100.0	138	4 AAB81977	Aab81977 Gangliosid
12	54	100.0	138	6 ABU11002	Abu11002 Modified
13	54	100.0	582	4 AAB81987	Aab81987 Gangliosid
14	54	100.0	582	4 AAB81991	Aab81991 Gangliosid
15	42	77.8	120	2 AAR34284	Aar34284 Human TNF
16	40	74.1	4130	8 ADQ26346	Adq26346 Chromobac
17	38	70.4	1781	5 ADU74519	Adu74519 Lactobact
18	37	68.5	94	7 ADF06503	Adf06503 Bacteriocl
19	37	68.5	137	7 ADC96455	Adc96455 E. faecili
20	37	68.5	179	6 ABO00524	Ab000524 Novel hum
21	37	68.5	232	8 ADN46177	Adn46177 Thermococ
22	37	68.5	380	4 AAE03835	Aae03835 Human gen
23	37	68.5	380	5 ABG64570	Abg64570 Human alb
24	37	68.5	380	8 ADL77837	Adl77837 Albumin F
25	37	68.5	388	5 ABP40106	Abp40106 Staphyloc

26	37	68.5	393	4 AAB88481	Aab88481 Human mem
27	37	68.5	685	7 ABO64573	Ab064573 Klebsiell
28	37	68.5	2022	6 ABR63232	AbR63232 Glucanase
29	36	66.7	160	5 ABR30519	Abp30519 Streptoco
30	36	66.7	163	5 ABR26309	Abp26309 Streptoco
31	36	66.7	257	3 AAG09510	Aag09510 Arabidops
32	36	66.7	257	3 AAG48547	Aag48547 Arabidops
33	36	66.7	258	8 ADN46472	Adn46472 Thermococ
34	36	66.7	260	3 AAG48546	Aag48546 Arabidops
35	36	66.7	260	3 AAG09509	Aag09509 Arabidops
36	36	66.7	354	3 AAG48543	Aag48543 Arabidops
37	36	66.7	361	4 AAB67540	Abb67540 Drosophi
38	36	66.7	361	4 AAB75213	Aab75213 Drosophi
39	36	66.7	361	5 AAB30515	Aae30515 Fruit fly
40	36	66.7	387	7 ADB70112	Adb70112 C. neofor
41	36	66.7	389	3 AAG48542	Aag48542 Arabidops
42	36	66.7	409	3 AAG48541	Aag48541 Arabidops
43	35	64.8	23	5 ABR46121	Abp46121 Human Bly
44	35	64.8	23	5 ABR47065	Abp47065 Human Bly
45	35	64.8	23	7 AAG97892	Adg97892 scfV VHC

ALIGNMENTS

RESULT 1
ID AAB81981 standard; peptide; 10 AA.
XX AAB81981;
AC
XX
DT 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related peptide SEQ ID NO: 5.
DE
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW Cancer.
KM
XX Mus musculus.
OS
XX WO200123432-A1.
PN
XX
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000MO-JP006774.
PF
XX
XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI WPI; 2001-266143/27.
DR
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Claim 5; Page 141; 183pp; Japanese.
PS
XX The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumors, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX
XX Sequence 10 AA:
SO
Query Match 100.0%; Score 54; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
 |||||
 XX
 DB 1 VKLGYTFDS 10

RESULT 2

ABU11006
 ID ABU11006 standard; peptide; 10 AA.
 XX
 AC ABU11006;

DT 04-FEB-2003 (first entry)
 XX
 DE Modified ganglioside GD3 antibody associated peptide #3.
 XX

KM Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 XX

OS Mus musculus.
 XX

PN W0200278739-A1.
 XX

PD 10-OCT-2002.
 XX

PF 29-MAR-2002; 2002WO-JP003170.
 XX

PR 29-MAR-2001; 2001JP-00097483.
 XX

PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX

PI Shitara K, Niwa R, Kanazawa J, Asada M;
 XX

DR WPI; 2003-067410/06.
 XX

PT Drug containing genetically-modified antibody against ganglioside GD3,
 its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX

PS Claim 6; Page 98; 121pp; Japanese.
 XX

CC The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a peptide associated with the anti- ganglioside GD3 antibody
 CC
 SQ Sequence 10 AA;

Query Match 100.0%; Score 54; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
 |||||
 DB 1 VKLGYTFDS 10

RESULT 3

AAB81985
 ID AAB81985 standard; protein; 119 AA.
 XX
 AC AAB81985;

DT 03-JUL-2001 (first entry)
 XX
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.
 XX

KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
 cancer.
 XX

OS Synthetic.
 XX

PN W0200123432-A1.
 XX

PD 05-APR-2001.
 XX

PF 29-SEP-2000; 2000WO-JP006774.
 XX

PR 30-SEP-1999; 99JP-00278291.
 XX

PR 06-APR-2000; 2000JP-00105088.
 XX

PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX

PI Hanai N, Shitara K, Nakamura K, Niwa R;
 XX

DR WPI; 2001-266143/27.
 XX

PT New human type complementation-determining region-transplanted antibody
 and derivatives against ganglioside GD3, useful in diagnosis and therapy
 of e.g. tumors, with low antigenicity, little side effects but potent
 activity in cancer.
 XX

PS Claim 20; Page 142-143; 183pp; Japanese.
 XX

CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumours, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 XX

SQ Sequence 119 AA;

Query Match 100.0%; Score 54; DB 4; Length 119;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
 |||||
 DB 99 VKLGYTFDS 108

RESULT 4

AAB81989
 ID AAB81989 standard; protein; 119 AA.
 XX

AC AAB81989;
 XX

DT 03-JUL-2001 (first entry)
 XX

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.
 XX

KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
 cancer.
 XX

OS Mus musculus.
 XX

PN W0200123432-A1.
 XX

PD 05-APR-2001.
 XX

PF 29-SEP-2000; 2000WO-JP006774.
 XX

PR 30-SEP-1999; 99JP-00278291.
 XX

PR 06-APR-2000; 2000JP-00105088.
 XX

PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX

PI Hanai N, Shitara K, Nakamura K, Niwa R;
 XX

DR WPI; 2001-266143/27.
 XX

PT New human type complementation-determining region-transplanted antibody
 and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.

PS Claim 10; Page 173-174; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX Sequence 119 AA;

Query Match 100.0%; Score 54; DB 4; Length 119;

Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKLGYTFDS 10
DB 99 VKLGYTFDS 108

RESULT 5
ABU1012

ID ABU1012 standard; protein; 119 AA.

XX ABU1012;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #5.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Mus musculus.

PN WO200278739-A1.

PD 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Shitara K, Niwa R, Kanazawa J, Asada M;

DR WPI; 2003-067410/06.

PT Drug containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.

PS Claim 7; Page 112-113; 121pp; Japanese.

CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX Sequence 119 AA;

Query Match 100.0%; Score 54; DB 6; Length 119;

Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKLGYTFDS 10
DB 99 VKLGYTFDS 108

DB 99 VKLGYTFDS 108

RESULT 6
ABU1010

ID ABU1010 standard; protein; 119 AA.

XX ABU1010;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #3.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Synthetic.

PN WO200278739-A1.

PD 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Shitara K, Niwa R, Kanazawa J, Asada M;

DR WPI; 2003-067410/06.

PT Drug containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.

PS Claim 8; Page 99; 121pp; Japanese.

CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX Sequence 119 AA;

Query Match 100.0%; Score 54; DB 6; Length 119;

Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKLGYTFDS 10
DB 99 VKLGYTFDS 108

RESULT 7
AAR3256

ID AAR3256 standard; protein; 130 AA.

XX AAR3256;

DT 25-MAR-2003 (revised)

PI 12-JUL-1993 (first entry)

DE Rat immunoglobulin H chain variable region of pXK641HA3.

XX Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;

XX humanised; chimeric; antibody; expression vector.

XX Rattus rattus.

```

FH Key Location/Qualifiers
FT Peptide 1..10
FT /note= "Signal peptide"
FT Protein 11..130
FT /note= "Mature protein"
XX
PN EP53199-A2.
XX
PD 24-MAR-1993.
XX
PF 18-SEP-1992; 92EP-00116026.
XX
PR 18-SEP-1991; 91JP-00238375.
XX
PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.
PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX
DR WPI, 1993-095510/12.
DR N-PSDB; AAO33257.
XX
PT Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
PT cancers, such as melanoma, neuroblastoma, etc.
XX
PS Claim 6; Page 29-30; 63pp; English.
XX
CC The sequences given in AAR33256-57 represent rat heavy and light chain
CC variable regions respectively. The DNA sequences encoding these proteins
CC were used in the construction of humanised chimeric antibody expression
CC vectors. In these humanised antibodies none of the amino acids of the non
CC -human animal Ab variable region have been changed. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 130 AA;

```

```

Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VKLGTYYFDS 10
Db 109 VKLGTYYFDS 118

```

```

RESULT 8
AAR53341
ID AAR53341 standard; protein; 130 AA.
XX
AC AAR53341;
XX
DT 18-NOV-1994 (first entry)
XX
DE KM641 L chain variable region.
XX
KM Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
KM expression vector; heavy; light; chain; hypervariable region; CDR;
KM constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /label= sig_peptide
XX
PN AU9346181-A.
XX
PD 17-MAR-1994.
XX
PF 07-SEP-1993; 93AU-00046181.
XX
PR 07-SEP-1992; 92JP-00238452.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.

```

```

XX
PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
XX
DR WPI; 1994-126857/16.
XX
DR N-PSDB; AAO45439.
XX
PT Humanised antibody specific for ganglioside GM2 - used for producing a
PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX
PS Example 2; Page 116-117; 191pp; English.
XX
CC Example 2 describes the construction of the vector pCh1641HA1 for
CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3
CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
CC AAO45438-39. A KM641-derived chimeric human Ab H chain expression vector
CC was constructed by joining the H chain variable region gene from
CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the
CC synthetic DNAs given in AAO63439 and AAO63440
XX
SQ Sequence 130 AA;

```

```

Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VKLGTYYFDS 10
Db 109 VKLGTYYFDS 118

```

```

RESULT 9
AAV28369
ID AAV28369 standard; protein; 130 AA.
XX
AC AAV28369;
XX
DT 04-NOV-1999 (first entry)
XX
DE pKM641 HA3 immunoglobulin heavy chain.
XX
KM antibody; nucleotide; genomic; hypervariable region; chimeric;
KM light chain; amino acid.
XX
OS Mus sp.
XX
PN US5939532-A.
XX
PD 17-AUG-1999.
XX
PF 07-JUN-1995; 95US-00483528.
XX
PR 07-SEP-1993; 93US-00116778.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
XX
DR WPI; 1999-468416/39.
DR N-PSDB; AAX99482.
XX
PT Chimeric human antibody expression vectors.
XX
PS Example 1; Col 99-101; 188pp; English.
XX
CC This immunoglobulin region was isolated from pKM641HA3. This sequence has
CC no methionine initiation codon and the leader sequence was partly
CC lacking. The chimeric human antibodies are useful in the treatment of
CC cancer, especially that which is of neural ectodermal origin. In contrast
CC to prior art constructs based on mouse monoclonal antibodies, the
CC chimeric human antibodies do not cause anti-mouse immunoglobulin
CC production. The chimeric human antibodies have a prolonged half-life and

```

CC a reduced frequency of adverse effects when compared to mouse monoclonal
 CC antibodies
 XX
 SQ Sequence 130 AA;

Query Match 100.0%; Score 54; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKLGYTFDS 10
 DB 109 VKLGYTFDS 118

RESULT 10
 AAB01627
 ID AAB01627 standard; protein; 130 AA.
 AC AAB01627;
 DT 07-DEC-2000 (first entry)
 DE Murine immunoglobulin heavy chain variable region.
 XX
 KW Mouse; immunoglobulin; H chain; heavy chain; variable region; cancer;
 XX humanised antibody.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT Peptide 1..10
 FT Protein /label= signal_peptide
 FT 11..130
 FT /label= mature_immunoglobulin_heavy_chain_variable region
 XX
 PN EP1013761-A2.
 PD 28-JUN-2000.
 XX
 PF 18-SEP-1992; 99EP-00124345.
 XX
 PR 18-SEP-1991; 91JP-00238375.
 PR 18-SEP-1992; 92EP-00116026.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
 XX
 DR WPI; 2000-402204/35.
 DR N-PSDB; AAS1003.
 PS
 PT New humanised chimera antibody KM-871 useful for treating cancer,
 PT comprises variable region of mouse monoclonal antibody, reactive with
 PT ganglioside and human antibody constant region.
 XX
 PS Claim 14; Page 27-28; 65pp; English.
 XX
 CC The present sequence is a murine immunoglobulin heavy chain variable
 CC region from plasmid KM-641. The coding sequence was used in the creation
 CC of an expression vector, along with the sequence for a human antibody, to
 CC produce humanised chimaeric antibodies, which can be used to treat
 CC cancer. Humanised chimaeric antibodies are more effective than mouse
 CC antibodies as they do not provoke a reaction in the human and side
 CC effects, such as the formation of anti-mouse immunoglobulin antibody and
 CC the rapid half-life of the immunoglobulins, do not occur
 XX
 SQ Sequence 130 AA;

Query Match 100.0%; Score 54; DB 3; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKLGYTFDS 10

DB 109 VKLGYTFDS 118

RESULT 11
 AAB81977
 ID AAB81977 standard; protein; 138 AA.
 AC AAB81977;
 DT 03-JUL-2001 (first entry)
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.
 XX
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
 XX cancer.
 OS Mus musculus.
 XX
 PN W0200123432-A1.
 PD 05-APR-2001.
 XX
 PF 29-SEP-2000; 2000WO-JP006774.
 XX
 PR 30-SEP-1999; 99JP-00278291.
 PR 06-APR-2000; 2000JP-00105088.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Hanai N, Shitara K, Nakamura K, Niwa R;
 XX
 DR WPI; 2001-266143/27.
 XX
 PT New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 PS Example 1; Page 138-139; 183pp; Japanese.
 XX
 CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 XX
 SQ Sequence 138 AA;

Query Match 100.0%; Score 54; DB 4; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKLGYTFDS 10
 DB 118 VKLGYTFDS 127

RESULT 12
 ABU1002
 ID ABU1002 standard; protein; 138 AA.
 AC ABU1002;
 DT 04-FEB-2003 (first entry)
 DE Modified ganglioside GD3 antibody associated protein #1.
 XX
 KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 XX
 OS Mus musculus.
 PN W0200278739-A1.

XX 10-OCT-2002.
PD
XX
XX 29-MAR-2002; 2002WO-JP003170.
PF
XX 29-MAR-2001; 2001JP-00097483.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Shitara K, Niwa R, Kanazawa J, Asada M;
PI
XX WPI; 2003-067410/06.
DR
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
XX Example 3; Page 97; 121pp; Japanese.
PS
XX The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 138 AA;
SQ
Query Match 100.0%; Score 54; DB 6; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VKLGTYYFDS 10
Db 118 VKLGTYYFDS 127
RESULT 13
AAB81987
ID AAB81987 standard; protein; 582 AA.
XX
AC AAB81987;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
XX Synthetic.
XX
XX WO200123432-A1.
PN
XX
XX 05-APR-2001.
PD
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX 30-SEP-1999; 99JP-00278291.
PR
XX 06-APR-2000; 2000JP-00105088.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI
XX WPI; 2001-266143/27.
DR
XX
XX New human type complementation-determining region-transplanted antibody
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
PT

XX Claim 41; Page 168-172; 183pp; Japanese.
PS
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX Sequence 582 AA;
SQ
Query Match 100.0%; Score 54; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VKLGTYYFDS 10
Db 99 VKLGTYYFDS 108
RESULT 14
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
XX Synthetic.
XX
XX WO200123432-A1.
PN
XX
XX 05-APR-2001.
PD
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX 30-SEP-1999; 99JP-00278291.
PR
XX 06-APR-2000; 2000JP-00105088.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI
XX WPI; 2001-266143/27.
DR
XX
XX New human type complementation-determining region-transplanted antibody
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
PT
XX Claim 39; Page 175-179; 183pp; Japanese.
PS
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX Sequence 582 AA;
SQ
Query Match 100.0%; Score 54; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VKLGTYYFDS 10
Db 99 VKLGTYYFDS 108

XX	AAK34284;
AC	25-MAR-2003 (revised)
XX	26-JUL-1993 (first entry)
DT	Human TNF binding antibody heavy chain VHLM2.
XX	Monoclonal antibody; anti-globulin response; VH gene; chimeric;
KW	mouse-human antibodies; antibody; prevention; tumour necrosis factor.
XX	Homo sapiens.
OS	
XX	
FH	Key
FT	Location/Qualifiers
FT	1..30
FT	/note= "Framework region FR1"
FT	31..35
FT	/note= "Complementarity determining region CDR1"
FT	36..49
FT	/note= "Framework region FR2"
FT	50..66
FT	/note= "Complementarity determining region CDR2"
FT	67..98
FT	/note= "Framework region FR3"
FT	99..116
FT	/note= "Complementarity determining region CDR3"
FT	117..120
FT	/note= "Framework region FR4"
XX	
XX	WO9306213-A1.
PB	01-APR-1993.
PF	23-SEP-1992;
XX	92WO-GB001755.
PR	23-SEP-1991;
PR	91GB-00020252.
PR	25-SEP-1991;
PR	91GB-00020377.
PR	24-MAR-1992;
PR	92GB-00006318.
PR	15-MAY-1992;
PR	92WO-GB000883.
PA	(MEDI-) MEDICAL RES COUNCIL.
PA	(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI	Hoogenboom HRJM, Baier M, Jespers LSAT, Winter GP;
PI	WPI; 1993-117534/14.
PT	Producing human antibody polypeptide dimer specific for antigen -
PT	comprises use of chain shuffling using phage expression, useful for
PT	reducing anti globulin responses in humans for increased human
PT	characteristics.
XX	
PS	Example; Fig 6; 109pp; English.
CC	The sequence is that of the heavy chain VHLM2 which shows minimal
CC	differences compared with the germline DP-46, which is of the VH3 family.
CC	It may be used as part of a method of producing chimeric mouse-human
CC	antibodies or fragments which have the same binding specificity as a
CC	parent Ab but have increased human characteristics, preventing anti-
CC	globulin response in humans. (Updated on 25-MAR-2003 to correct PN
CC	field.)
XX	
SQ	Sequence 120 AA;
Query Match	77.8%; Score 42; DB 2; Length 120;
Best Local Similarity	87.5%; Pred. No. 4,6;
Matches	7; Conservative 1; Mismatches 0; Indels 0; Gaps 0

3 LGTYFDS 10
 |||||
 Db 101 LGTYFDS 108
 RESULT 16
 ID ADO26346
 ADO26346 standard; protein; 4130 AA.
 AC ADO26346;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Chromobacterium violaceum CV44287 involved in haemolysin synthesis.
 XX
 KM Haemolysin; anticoagulant; CV44287.
 XX
 OS Chromobacterium violaceum.
 XX
 PN MO2004056960-A2.
 XX
 PD 08-JUL-2004.
 XX
 PF 16-DEC-2003; 2003WO-BR00207.
 XX
 PR 19-DEC-2002; 2002BR-00007239.
 XX
 PA (CNPQ-) CNPQ CONSELHO NACIONAL DESENVOLVIMENTO.
 XX
 De Vasconcelos ATR, Simpson AJG, Abreu HNS, De Almeida DF;
 PI Almeida FC, De Almeida R, Anticono RV, Araride JR, De Araujo MFF;
 PI Bogo RM, Bonatto SL, Brígido MDW, De Brito CPA, Brochi M, Burity HA;
 PI Carneiro A, Carraro D, Carvalho CMB, Cascardo JCM, Cavada BS;
 PI Chneirg LMDO, Da Cunha MH, Fantinatti F, Farias IP, Felipe MSS;
 PI Ferrari LP, Ferro JA, Franco GR, De Freitas NSA, Furian LR;
 PI Gattapaglia D, Gazzinelli RT, Gomes JAA, Gonçalves PR, Grangeiro TB;
 PI Girdard EC, Guimarães CT, Hanna ES, Jardim SN, Laurino JP, Lima LFA;
 PI De Lyra MCCP, Madeira HM, Maranhão AO, Manfio GP, Martins WS;
 PI De Medeiros SRB, Meisener RDV, Moreira MA, Do Nascimento FF;
 PI Nicollas MP, De Oliveira UG, Oliveira SC, Paixão RFC, Parra J;
 PI Paes TBC, Petrosa FDO, Pena SDB, Pereira JO, Pereira M, Pinto LSRG;
 PI Pinto LDS, Porto JR, Potrich DP, Ramalho CE, Reis AMM;
 PI Rondinelli E, Sampaio AH, Dos Santos FR, Schneider MPC, Silva DW;
 PI Silva R, Soares CMA, De Souza EM, De Souza KRL, Souza RC;
 PI Steindel M, Teixeira SMR, Trevilato PB, Uruenyl TP, Wassen R;
 PI Azevedo V, Barcellet LA, Batista JDS, Filho AS, Zaha A;
 PI Andrade EDMF, Gonzaga L, Dos Santos EBP, Soares RDBB, Batuas LAM;
 PI Cardoso DEDP, Parente JA, Rigo LU, Steffens MBR;
 XX
 WPI, 2004-500292/47.
 XX
 New gene-coding polynucleotides of the chromosome of Chromobacterium
 PT violaceum, useful for therapeutic, diagnostic or pharmacological
 PT applications, in control processes for environmental parameters or in
 PT enzyme syntheses.
 XX
 PS Claim 4; SEQ ID NO 19; 31pp; English.
 XX
 The present sequence is that of the protein encoded by the CV44287 gene
 CC of Chromobacterium violaceum strain ATCC 12472 (NCIB 9131, NCTC 9757, JCM
 CC 1249, DSM 30191, IAM 12470, LMG 1267). The invention relates to 29
 CC polynucleotides that have been identified by sequencing the genome of
 CC this strain, to the polypeptides ADO26348-AO26356 encoded by these
 CC polynucleotides, and to the uses of the polynucleotides and polypeptides
 CC for therapeutic, diagnostic, medicinal, pharmacological and
 CC pharmacognostic applications, in control processes for environmental
 CC parameters, and in enzyme synthetic processes. The CV44287 gene is
 CC involved in haemolytic activity. The gene and the encoded polypeptide can
 CC be used in the production of haemolysins for pharmaceutical use as
 CC anticoagulants.
 XX
 Sequence 4130 AA;
 SQ

Query Match 74.1%; Score 40; DB 8; Length 4130;
 Best Local Similarity 70.0%; Pred. No. 5.3e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10
 |||::|||
 Db 2460 VKLGTTFHFD 2469

RESULT 17
 AAU74519
 ID AAU74519 standard; protein; 1781 AA.
 AC AAU74519;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Lactobacillus reuteri glucosyltransferase A (gtfa) polypeptide.
 XX
 KM Glucosyltransferase A; gtfa; glucan; anhydroglucose; sucrose;
 KM oligosaccharide; polysaccharide; sucrose; fructan; symbiotic; probiotic.
 XX
 OS Lactobacillus reuteri.
 XX
 PN W0200190372-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001; 2001MO-NL000393.
 XX
 PR 25-MAY-2000; 2000EP-00201871.
 XX
 PA (NEDE) NEDERLANDSE ORG TOEGEPAST.
 XX
 PI Van Geel Schutten GH, Dijkhuizen L, Rahaoui H, Leer RJ;
 DR WPI; 2002-147583/19.
 DR N-PSDB; AAS20540.
 XX
 PT Protein with glucosyltransferase activity derived from Lactobacillus
 PT Reuteri.
 XX
 PS Claim 3; Page 48-55; 59pp; English.
 XX
 CC The invention relates to a Lactobacillus reuteri glucosyltransferase A
 CC (gtfa) polypeptide. This polypeptide produces a glucan with a unique
 CC structure having 4-linked, 6-linked and 4,6-linked anhydroglucose units
 CC or, in the presence of suitable acceptors, oligosaccharides. The protein
 CC can be used to produce an oligosaccharide or polysaccharide of interest,
 CC for example, to produce a glucan with sucrose as a substrate and
 CC optionally a fructan as a probiotic or symbiotic. This sequence
 CC represents L. reuteri glucosyltransferase A
 CC
 XX
 SO Sequence 1781 AA;

Query Match 70.4%; Score 38; DB 5; Length 1781;
 Best Local Similarity 85.7%; Pred. No. 5.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFDS 10
 |||||:
 Db 1724 GTYYFDN 1730

RESULT 18
 ADF06503
 ID ADF06503 standard; protein; 94 AA.
 XX
 AC ADF06503;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Bacterial polypeptide #2616.

XX
 KM Proteus mirabilis infection; bacterial infection; antibacterial;
 KM Immunostimulant.
 XX
 OS Proteus mirabilis.
 XX
 PN US6605709-B1.
 XX
 PD 12-AUG-2003.
 XX
 PF 05-APR-2000; 2000US-00543681.
 XX
 PR 09-APR-1999; 99US-0128706P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Breton GL;
 XX
 DR WPI; 2003-895291/82.
 DR N-PSDB; ADF02331.
 XX
 PT New Proteus mirabilis polypeptides and polynucleotides, useful as
 PT reagents for diagnosis of bacterial disease, as components of
 PT antibacterial vaccines, as targets for antibacterial drugs, or as
 PT biocontrol agents for plants.
 XX
 PS Disclosure; SEQ ID NO 6788; 870pp; English.
 XX
 CC The invention relates to new Proteus mirabilis polypeptides and
 CC polynucleotides. The invention also relates to antibodies against the
 CC polypeptides, methods for producing the polypeptides, a method of
 CC generating vaccines for immunising an individual against P. mirabilis, a
 CC method for evaluating a compound for the ability to bind a P. mirabilis
 CC polypeptide and a method for screening test compounds for anti-bacterial
 CC activity. The polypeptides and polynucleotides are useful as molecular
 CC targets for diagnosing, preventing and treating pathological conditions
 CC resulting from bacterial infection, as reagents for diagnosis of
 CC bacterial diseases, as components of antibacterial vaccines, as targets
 CC for antibacterial drugs or as bio-control agents for plants. This
 CC sequence represents a Proteus mirabilis polypeptide of the invention.
 XX
 SO Sequence 94 AA;

Query Match 68.5%; Score 37; DB 7; Length 94;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
 |||||:
 Db 21 LGTYFNS 28

RESULT 19
 ADC96455
 ID ADC96455 standard; protein; 137 AA.
 XX
 AC ADC96455;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE E. faecium protein sequence SEQ ID 6082.
 XX
 KM Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 KM abdominal-pelvic infection.
 XX
 OS Enterococcus faecium.
 XX
 PN US6583275-B1.
 XX
 PD 24-JUN-2003.
 XX
 PF 30-JUN-1998; 98US-00107532.
 XX

PR 02-JUL-1997; 97US-0051571P.
 PR 14-MAY-1998; 98US-0085598P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Doucette-Stamm LA, Bush D;
 XX
 DR WPI: 2003-799836/75.
 DR N-PSDB; ADC92801.
 XX
 PT New isolated nucleic acid derived from *Enterococcus faecium* encoding an
 PT *Enterococcus faecium* polypeptide useful for detection, prevention and
 PT treatment of a pathological condition resulting from a bacterial
 PT infection.
 PS
 PS Example 1; SEQ ID NO 6082; 243bp; English.
 XX
 XX The invention relates to an isolated nucleic acid derived from
 CC *Enterococcus faecium* encoding an *Enterococcus faecium* polypeptide having
 CC one of 10 fully defined sequences given in the (or comprising 40
 CC sequential nucleotides chosen from any of the nucleic acids, its
 CC complement or sequences hybridising to it). Also included are a
 CC recombinant vector comprising the nucleic acid operably linked to
 CC transcription regulatory element, a cell comprising the vector and a
 CC single-stranded probe comprising the nucleic acid. The nucleic acids are
 CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
 CC The nucleic acids is useful for diagnosing pathological conditions
 CC resulting from *E. faecium* bacterial infection (e.g. urinary tract
 CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
 CC infection) and for screening drugs such as agonists and antagonists. The
 CC nucleic acid is useful for recombinant production of *Candida albicans* -
 CC derived peptides or antisense polypeptides. Pharmaceutical compositions
 CC and vaccines containing the nucleic acid are useful for preventing or
 CC treating *Enterococcus faecium* infections. The present sequence represents
 CC one if the disclosed *E. faecium* proteins.
 CC
 XX
 SQ Sequence 137 AA;
 Query Match 68.5%; Score 37; DB 7; Length 137;
 Best Local Similarity 75.0%; Pred. NO. 48;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
 QY 2 KLCGYTYPD 9
 |:|:|:|:|
 DB 124 KIGTYTYPD 131
 RESULT 20
 ID ABO00524 standard; protein, 179 AA.
 AC ABO00524;
 XX
 XX 06-AUG-2003 (first entry)
 DT
 DT Novel human polypeptide #111.
 DE
 DE Human; angiogenesis; cytokine; cell proliferation; pluripotent;
 KM cell differentiation; totipotent; stem cell; transplantation; bio-sensor;
 KM neuroepithelial cell; autoimmune disease; neural cell; genetic disorder;
 KM nerve; brain tissue; central nervous system disease;
 KM peripheral nervous system disease; neuropathy; haematopoiesis; bone;
 KM myeloid disorder; lymphoid cell disorder; platelet disorder; tendon;
 KM regeneration; cartilage; tendon; ligament; nerve tissue growth;
 KM tissue repair; wound healing; burn; ulcer; osteoporosis; cancer;
 KM osteoarthritis; bone degenerative disorder; periodontal disease;
 KM gut protection; lung fibrosis; liver fibrosis; reperfusion injury;
 KM immune deficiency; infection; autoimmune disorder; allergic reaction;
 KM thrombolytic; thrombosis; coagulation disorder; hereditary disorder;
 KM biocytin; circadian cycle; fertility; metabolism; catabolism; anabolism;
 KM neurologic; neuroprotective; antiparkinsonian; anticonvulsant;
 KM haemostatic; vulnerary; antiulcer; osteopathic; antiarthritic;
 KM vasotrophic; immunostimulant; antibacterial; fungicide; immunosuppressive;
 KM

XX anti-rheumatic; anti-diabetic; antislathmatic; cytostatic; virocidic.
XX
XX Homo sapiens.
XX
XX WO2003023013-A2.
XX
XX 20-MAR-2003.
XX
XX
XX 13-SEP-2002; 2002WO-US029001.
XX
XX
XX 13-SEP-2001; 2001US-0322511P.
XX
XX 12-SEP-2002; 2002US-00243552.
XX
XX (HYSE-) HYSEQ INC.
XX
XX
XX Tang YT, Yang Y, Wang Z, Wang G, Ma Y;
XX
XX WPI; 2003-313249/30.
XX
XX N-PSDB; ACD05601.
XX
XX
XX Novel nucleic acids and polypeptides for diagnosis, treatment of central
XX and peripheral nervous system diseases and neuropathies, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis.
XX
XX
XX Claim 20; SEQ ID NO 447; 300pp; English.
XX
XX
XX The present invention relates to the isolation of novel human
XX polynucleotide sequences and their encoding polypeptides. The novel
XX polypeptides exhibit activities relating to angiogenesis, cytokine, cell
XX proliferation, cell differentiation, antiinflammatory, and stem cell
XX growth factor activities. The polypeptides are involved in the
XX proliferation, differentiation and survival of pluripotent and totipotent
XX stem cells, and are useful for re-engineering damaged or diseased
XX tissues, transplantation, manufacture of bio-pharmaceuticals and
XX development of bio-sensors. The polypeptides can be used to manipulate
XX stem cells in culture to give rise to neuroepithelial cells that can be
XX used to augment or replace cells damaged by illness, autoimmune disease,
XX accidental damage or genetic disorders. The polypeptides induce the
XX proliferation of neural cells and regeneration of nerve and brain tissue
XX and are useful for the treatment of central and peripheral nervous system
XX diseases and neuropathies, such as Alzheimer's, Parkinson's disease,
XX Huntington's disease, amyotrophic lateral sclerosis (ALS). The
XX polypeptides are also involved in chemotactic or chemokinetic activity,
XX regulation of haematopoiesis and are useful for treating myeloid or
XX lymphoid cell disorders, platelet disorders such as thrombocytopenia and
XX for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
XX growth, in tissue repair, healing of burns, incisions, ulcers, for
XX treating osteoporosis, osteoarthritis, bone degenerative disorders, and
XX periodontal disease. The polypeptides are also useful for gut protection
XX or regeneration and treatment of lung or liver fibrosis, reperfusion
XX injury in various tissues, various immune deficiencies and disorders
XX including severe combined immunodeficiency (SCID), bacterial or fungal
XX infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid
XX arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and
XX conditions, such as asthma or other respiratory problems. The
XX polypeptides are involved in thrombolytic or thrombotic and are useful in
XX treatment of various coagulation disorders (including hereditary
XX disorders such as haemophilia) or to enhance coagulation and other
XX haemostatic events in treating wounds resulting from trauma, surgery or
XX other causes. The polypeptides exhibit immune stimulating or immune
XX suppressing activity, and are useful for treating autoimmune diseases or
XX cancer. They also inhibit the growth, infection or function of infectious
XX agents such as bacteria, fungi, viruses, effect biorythms or circadian
XX cycles of rhythms, fertility of male or female subjects, metabolism,
XX catabolism, and anabolism. ABO00414-ABO00749 represent the novel
XX polypeptides of the invention. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WPI at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 179 AA;
XX

Query Match 68.5%; Score 37; DB 6; Length 179;
Best Local Similarity 87.5%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 LGTYFPDS 10
Db 150 LGTYSDS 157

RESULT 21
ADN46177
ID ADN46177 standard; protein; 222 AA.
XX
AC ADN46177;
XX
DT 01-JUL-2004 (first entry)
XX
DE Thermococcus kodakaraensis KOD1 protein sequence SegID55.
XX
KW gene disruption; gene targeting; marker gene; transformation;
KW homologous recombination; hyperthermostable archaeobacterium; KOD1;
KW gene structure; gene function; enzyme activity; medicine;
KW forensic science; food; drug inspection; molecular biology; immunology.
XX
OS Thermococcus kodakaraensis.
XX
PN WO2004022736-A1.
XX
PD 18-MAR-2004.
XX
PF 29-AUG-2003; 2003WO-1B003597.
XX
PR 30-AUG-2002; 2002JP-00319011.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Imanaka T, Atomi H;
XX
DR WPI; 2004-257583/24.
XX
PT Method for disrupting targeted gene in genome of organism particularly
PT thermostable bacterium and with genome chips for analysis, applicable in
PT studying gene structure and functions.
XX
PS Claim 9; SEQ ID NO 55; 538bp; Japanese.
XX
XX
CC This invention relates to a novel method for targeting disruption of an
CC arbitrary gene in a genome of an organism which comprises providing the
CC whole sequential data of the genome of such organism, selecting at least
CC 1 arbitrary region in the sequence, providing a vector that contains a
CC sequence homologous with the selected region and a marker gene,
CC transformation, and homologous recombination. The genome is preferably
CC the genome of a hyperthermostable archaeobacterium, particularly
CC Thermococcus kodakaraensis KOD1. The method is for targeting the
CC disruption of a gene in the genome of an organism, which is applicable in
CC studying gene structure and functions as well as enzyme activities of
CC encoded proteins and useful in medicine, forensic science, food or drug
CC inspection, molecular biology and immunology. With this method, the
CC disruption of a gene at an arbitrary position in a genome can be achieved
CC efficiently and reliably. The present sequence is that of a protein
CC encoded by the genome of Thermococcus kodakaraensis which was derived
CC using the method of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 222 AA;

Query Match 68.5%; Score 37; DB 8; Length 222;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 VKLGTYFPDS 10

Db 145 VKLGTYVYDT 154
:|||||:|
AAE03835
ID AAE03835 standard; protein; 380 AA.
XX
AC AAE03835;
XX
DT 08-AUG-2001 (first entry)
XX
DE Human gene 18 encoded secreted protein HRKM50, SEQ ID NO: 81.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW inflammation; neurological disorder; Alzheimer's disease; food additive;
KW angiotensin disorder; kidney disorder; gastrointestinal disorder; allergy;
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW cell culture; chemotaxis; vulnerability; binding partner identification;
KW gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..380
FT /note= "Mature secreted protein"
XX
PN WO200136440-A1.
XX
PD 25-MAY-2001.
XX
PF 15-NOV-2000; 2000WO-US031282.
XX
PR 19-NOV-1999; 99US-0166414P.
XX
PR 21-JUL-2000; 2000US-0219665P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Komatsoulis GA, Birse CE, Moore PA;
XX
DR WPI; 2001-343795/36.
XX
DR N-PSDB; AAD08360.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is used
PT in preventing, treating or ameliorating a medical condition.
XX
XX
PS Claim 11; Page 496-498; 553bp; English.
XX
CC AAD08283-AAD08355 represent cDNAs corresponding to 23 human secreted
CC protein genes, and AAE03818-AAE03870 represent the proteins they encode.
CC AAE03871-AAE03896 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 23 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, disease),
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell

CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or
 CC preservative to modify storage properties. Antibodies specific for a
 CC protein of the invention can be used in alleviating symptoms associated
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
 CC present sequence represents a human secreted protein of the invention
 XX

SO Sequence 380 AA;

Query Match 68.5%; Score 37; DB 4; Length 380;
 Best Local Similarity 87.5%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYYPDS 10
 DB 183 LGTYYSDS 190

RESULT 23

ABG64570
 ID ABG64570 standard; protein; 380 AA.

AC ABG64570;

DT 27-AUG-2002 (first entry)

DE Human albumin fusion protein #1245.

XX Albumin fusion protein; therapeutic protein X; human albumin; HA;
 KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytostatic; antileukemia; antiinflammatory; antitumor;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic.

OS Homo sapiens.
 OS Synthetic.

PN WO200177137-A1.

PD 18-OCT-2001.

PF 12-APR-2001; 2001WO-US011988.

PR 12-APR-2000; 2000US-0229358P.

PR 25-APR-2000; 2000US-0199384P.

PR 21-DEC-2000; 2000US-0256931P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Haseltine WA;

PI MPI; 2002-010886/01.

PT New fusion protein for treating disease e.g. diabetes comprises an

PT albumin fused to a therapeutic protein.

PS Claim 1; Page 1335-1336; 2102pp; English.

XX The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or disorder
 CC that may be modulated by therapeutic protein X. The albumin extends the
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo
 CC activity. The protein is useful for treating and diagnosing disorders
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
 CC disease, ulcerative colitis), immune disorders (e.g. acquired
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),

CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
 CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
 XX

SO Sequence 380 AA;

Query Match 68.5%; Score 37; DB 5; Length 380;
 Best Local Similarity 87.5%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYYPDS 10
 DB 183 LGTYYSDS 190

RESULT 24

ADL77837
 ID ADL77837 standard; protein; 380 AA.

AC ADL77837;

DT 20-MAY-2004 (first entry)

DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1319.

XX albumin fusion protein; cytostatic; antianaemic; antiarthritic;
 KW antiaesthetic; anti-HIV; immunosuppressive; antiinflammatory;
 KW antipneumatic; antibacterial; osteopathic; dermatological; antigout;
 KW immunomodulator; antiarrhythmic; cardiac; neurotropic; antilipemic;
 KW nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;
 KW antidiabetic; anabolic; hypertensive; vulnery; gene therapy; cancer;
 KW reproductive system disorder; therapeutic protein.

XX Unidentified.

PN US2004010134-A1.

PD 15-JAN-2004.

PF 12-APR-2001; 2001US-00833245.

PR 12-APR-2000; 2000US-0229358P.

PR 25-APR-2000; 2000US-0199384P.

PR 21-DEC-2000; 2000US-0256931P.

PA (ROSE/) ROSEN C A.

PI (HASE/) HASELTINE W A.

PI Rosen CA, Haseltine WA;

PI MPI; 2004-090519/09.

PT New albumin fusion proteins, useful for diagnosing, treating, preventing

PT or ameliorating diseases or disorders e.g. cancer, anemia, arthritis,
 CC asthma, inflammatory bowel disease or Alzheimer's disease.

PS Disclosure; SEQ ID NO 1319; 279pp; English.

XX The invention relates to a novel albumin fusion protein. The invention
 CC further relates to: a composition comprising the albumin fusion protein
 CC and a pharmaceutical carrier; a kit comprising the composition of the
 CC albumin fusion protein formula; a method of treating a disease or
 CC disorder in a patient comprising the step of administering the albumin
 CC fusion protein; a method of treating a patient with a disease or disorder
 CC that is modulated by Therapeutic Protein X, or its fragment or variant;
 CC a method of extending the shelf life of Therapeutic Protein X, or its
 CC fragment or variant; a nucleic acid molecule comprising a polynucleotide
 CC sequence encoding the albumin fusion protein; a vector comprising the
 CC nucleic acid molecule of the albumin fusion protein; and a host cell
 CC comprising the nucleic acid molecule of the albumin fusion protein. The
 CC albumin fusion protein and its compositions have the following
 CC activities: cyostatic, antianaemic, antiarthritic, antiaesthetic, anti-

CC HIV, immunosuppressive, antiinflammatory, antipsoriatic, antibacterial,
 CC osteopathic, dermatological, antigout, immunomodulator, antiarhythmic,
 CC cardant, nootropic, antidiabetic, nephrotropic, uropathic,
 CC neuroprotective, antiparinsonian, tranquilizer, antidiabetic, anabolic,
 CC hypertensive, and vulnerary. The albumin fusion protein nucleic acid may
 CC be used in gene therapy to treat disorders. The albumin fusion protein is
 CC useful for diagnosing, treating, preventing or ameliorating diseases or
 CC disorders comprising indication: Y. The diseases or disorders include:
 CC cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer),
 CC immune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, acute
 CC lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,
 CC autoimmune disease, inflammatory bowel disease, psoriasis or Lyme
 CC disease), reproductive system disorders (e.g. prostatitis, inguinal
 CC hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-
 CC Leydig tumours), musculoskeletal diseases (e.g. giant cell tumours,
 CC Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy
 CC or cachexia), cardiovascular disease (e.g. rhabdomyoma, heart disease,
 CC arrhythmia, cardiac arrest, heat valve disease, hypernatraemia or
 CC hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome, or
 CC Down's syndrome, Patau syndrome, Turner's syndrome, Apert syndrome or Tay-
 CC Sachs disease), excretory diseases (e.g. urinary incontinence, urinary
 CC tract infections or renal disorders), neural or sensory disease (e.g.,
 CC Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis,
 CC cerebellar ataxia, attention deficit disorder, autism or obsessive
 CC compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or
 CC occupational lung disease), endocrine diseases (e.g. diabetes, Addison's
 CC disease or glomerulonephritis), digestive diseases (e.g. portal
 CC hypertension, irritable bowel disease, gastric atrophy or pancreatitis)
 CC or connective tissue or epithelial diseases (e.g. Crohn's disease,
 CC scleroderma, wound healing or epidermolysis bullosa). This sequence
 CC represents a therapeutic protein X relating to the albumin fusion protein
 CC of the invention. The sequence listing data for this specification was
 CC downloaded from the USPTO website.

SO Sequence 380 AA;

Query Match 68.5%; Score 37; DB 8; Length 380;
 Best Local Similarity 87.5%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
 Db 183 LGTYSDS 190

RESULT 25

ABP40106
 ID ABP40106 standard; protein; 388 AA.

AC ABP40106;

DT 24-JUL-2002 (first entry)

DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4951.

KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 anti-bacterial; gene therapy.

OS Staphylococcus epidermidis.

PN US6380370-B1.

PD 30-APR-2002.

PF 13-AUG-1998; 98US-00134001.

PR 14-AUG-1997; 97US-0055779P.

PR 08-NOV-1997; 97US-0064964P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Doucette-Stamm LA, Bush D;

XX

DR WPI, 2002-381255/41.
 DR N-PSDB; AAB92651.
 XX
 PT Novel isolated nucleic acid encoding a Staphylococcus epidermis
 PT polypeptide, useful for diagnosing and treating bacterial infections.
 XX
 PS Disclosure; SEQ ID NO 4951; 267pp; English.

XX AABN90538 to AABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in AABP35124 to AABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences can
 CC also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life cycle
 CC or inhibit S. epidermidis infection. N.B. The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site

SO Sequence 388 AA;

Query Match 68.5%; Score 37; DB 5; Length 388;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYFDS 10
 Db 250 RVGTYFGS 258

RESULT 26

AAB88481
 ID AAB88481 standard; protein; 393 AA.

AC AAB88481;

DT 23-MAY-2001 (first entry)

DE Human membrane or secretory protein clone PSBC0251.

KW Human; secretory protein; membrane protein; vaccine; gene therapy;
 rheumatoid arthritis; diabetes.

OS Homo sapiens.

PN EP1067182-A2.

PD 10-JAN-2001.

PF 07-JUL-2000; 2000EP-00114090.

PR 08-JUL-1999; 99GP-00194179.

PR 11-JAN-2000; 2000JP-00118775.

PR 02-MAY-2000; 2000JP-00183766.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

DR WPI, 2001-093989/11.

DR N-PSDB; AAF93908.

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 gene therapy or as candidate target molecules in drug development.

PS Claim 1; SEQ ID NO 330; 609pp + Sequence Listing; English.

XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by AAB88317
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
 CC invention. The invention also includes methods for the production of the
 CC antibodies directed against the proteins, and cDNA sequences, which can

be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). Examples of diseases which may be treated include rheumatoid arthritis and diabetes

SQ Sequence 393 AA;

Query Match Score 37; DB 4; Length 393;

Best Local Similarity 87.5%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYYPDS 10

Db 196 LGTYYPDS 203

RESULT 27

ABO64573

ID ABO64573 standard; protein; 685 AA.

AC ABO64573;

XX 29-JUL-2004 (first entry)

DE Klebsiella pneumoniae polypeptide seqid 11090.

KM Recombinant expression vector; transcription regulatory element;

XX Klebsiella pneumoniae protein; antibacterial; Vaccine.

OS Klebsiella pneumoniae.

XX US6610836-B1.

PD 26-AUG-2003.

XX 27-JAN-2000; 2000US-00489039.

PR 29-JAN-1999; 99US-0117747P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Breton GL, Osborne M;

DR MPI; 2003-895346/82.

N-PSDB; ACH98124.

New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.

Discloure; SEQ ID NO 11090; 932pp; English.

The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a

Klebsiella pneumoniae polypeptide of the invention

Sequence 685 AA;

Query Match Score 37; DB 7; Length 685;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTFYPDS 10

Db 577 GTFYPDS 583

RESULT 28

ID ABR63232 standard; protein; 2022 AA.

AC ABR63232;

XX 27-AUG-2003 (first entry)

DE Glucansucrase sequence from strain ML1.

KM Glucan; glucosyltransferase activity; thickener; prebiotic;

XX bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.

OS Lactobacillus reuteri.

XX WO2003008618-A2.

PD 30-JAN-2003.

XX 22-JUL-2002; 2002WO-NL000495.

PR 20-JUL-2001; 2001EP-00202752.

XX 25-JUL-2001; 2001EP-00202841.

PA (NED) NEDERLANDSE ORG TOEGEPAST.

PI Van Geel - Schutten GH;

DR MPI; 2003-289780/28.

N-PSDB; ACC64448.

Novel glucan produced by glucosyltransferase activity of lactic acid bacterium on sucrose substrate, and having backbone consisting of alpha (1,3)- and alpha (1,6)-linked anhydroglucose units, useful as thickener.

Claim 11; Fig 1; 51pp; English.

The present invention relates to glucan capable of being produced by glucosyltransferase activity of a lactic acid bacterium on a sucrose substrate. The method is useful as a thickener, as a prebiotic and as a bioactive agent and as an anti-corrosion agent. The glucan can be incorporated in foodstuffs such as beverages, sauces, dressings, dairy products. The glucan is useful as anticorrosion agent, e.g. for the protection of ship hulls. It can also be incorporated in nutritional or pharmaceutical compositions intended for improving the condition of the gastrointestinal tract. The present sequence represents a sequence of the glucansucrase gene

Sequence 2022 AA;

Query Match Score 37; DB 6; Length 2022;

Best Local Similarity 72.7%; Pred. No. 9.1e+02;

Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 VKLG--TYFPD 9

Db 1724 VKIGMDTYFPD 1734

RESULT 29

ID ABR30519 standard; protein; 160 AA.

XX

AC	ABP30519;
XX	
DT	02-JUL-2002 (first entry)
DE	Streptococcus polypeptide SEQ ID NO 10214.
KM	Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW	group A streptococcus; Streptococcus pyogenes; antibacterial;
KX	antiinflammatory; infection; vaccine; meningitis; gene therapy.
OS	Streptococcus agalactiae.
XX	
PN	MO200234771-A2.
PD	02-MAY-2002.
PF	29-OCT-2001; 2001WO-GB004789.
PR	27-OCT-2000; 2000GB-00026333.
PR	24-NOV-2000; 2000GB-00028727.
XX	07-MAR-2001; 2001GB-00005640.
PA	(CHIR-) CHIRON SPA.
PA	(GENO-) INST GENOMIC RES.
P1	Telford J, Maignani V, Margarit y Rosl, Grandi G, Fraser C;
P1	Tetteijn H;
DR	WI: 2002-352536/38.
DR	N-PDB: ABN71150.
XX	
PT	New Streptococcus protein for the treatment or prevention of infection or
PT	disease caused by Streptococcus bacteria, such as meningitis, and for
PT	detecting a compound that binds to the protein.
XX	
PS	Claim 1; Page 4151; 4525pp; English.
CC	The invention relates to a protein (ABP25413-ABP30895) from group B
CC	streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC	(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC	the specification. The proteins have antibacterial and antiinflammatory
CC	activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC	antibodies that bind (I) are used in the manufacture of medicaments for
CC	the treatment or prevention of infection or disease caused by
CC	Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC	Nucleic acids encoding (I) are used to detect Streptococcus in a
CC	biological sample. (I) is used to determine whether a compound binds to
CC	(I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC	used as a vaccine or diagnostic composition. The disease caused by
CC	Streptococcus that is prevented or treated may be meningitis. Nucleic
CC	acid encoding (I) may be used to recombinantly produce (I) and may be
CC	used in gene therapy. Antibodies to (I) are used for affinity
CC	chromatography, immunoassays, and distinguishing/identifying
CC	Streptococcus proteins
XX	
SQ	Sequence 160 AA:
OY	
Db	2 KLGTGYFPD 9 : 110 ELGRTYFP 117
RESULT 30	
ID	ABP26309
XX	ABP26309 standard; protein; 163 AA.
AC	ABP26309;
XX	
DT	02-JUL-2002 (first entry)

XX	Streptococcus	polypeptide SEQ ID NO 1794.
DE		
XX	Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;	
KM	group A streptococcus; Streptococcus pyogenes; antibacterial;	
KM	antiinflammatory; infection; vaccine; meningitis; gene therapy.	
XX		
OS	Streptococcus agalactiae.	
XX		
PN	WO200234771-A2.	
XX		
PD	02-MAY-2002.	
XX		
PF	29-OCT-2001; 2001WO-GB004789.	
XX		
PR	27-OCT-2000; 2000GB-00026333.	
PR	24-NOV-2000; 2000GB-00028727.	
XX	07-MAR-2001; 2001GB-00005640.	
XX		
PA	(CHIR-) CHIRON SPA.	
PA	(GENO-) INST GENOMIC RES.	
PI	Telford J, Masignani V, Margarit Y Rosl, Grandi G, Fraser C;	
PI	Tettelin H;	
DR	WPI; 2002-352536/38.	
DR	N-PSDB; ABN66940.	
PT	New Streptococcus protein for the treatment or prevention of infection or	
PT	disease caused by Streptococcus bacteria, such as meningitis, and for	
PT	detecting a compound that binds to the protein.	
XX		
PS	Claim 1; Page 3329; 4525PP; English.	
XX		
XX	The invention relates to a protein (ABP25413-ABP30895) from group B	
CC	streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS	
CC	(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in	
CC	the specification. The proteins have antibacterial and antiinflammatory	
CC	activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and	
CC	antibodies that bind (1) are used in the manufacture of medicaments for	
CC	the treatment or prevention of infection or disease caused by	
CC	Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.	
CC	Nucleic acids encoding (1) are used to detect Streptococcus in a	
CC	biological sample. (1) is used to determine whether a compound binds to	
CC	(1). A composition comprising (1) or a nucleic acid encoding (1), may be	
CC	used as a vaccine or diagnostic composition. The disease caused by	
CC	Streptococcus that is prevented or treated may be meningitis. Nucleic	
CC	acid encoding (1) may be used to recombinantly produce (1) and may be	
CC	used in gene therapy. Antibodies to (1) are used for affinity	
CC	chromatography, immunoassays, and distinguishing/identifying	
CC	Streptococcus proteins	
XX		
XX		
SQ	Sequence 163 AA;	
QY	2 KLGTYYPD 9	
	:	
DB	113 ELGGEYFD 120	
	66.7%; Score 36; DB 5; Length 163;	
	Best Local Similarity 75.0%; Pred. No. 90;	
	Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
RESULT 11		
AA609510		
ID	AA609510 standard; protein; 257 AA.	
AC	AA609510;	
XX		
DT	17-OCT-2000 (first entry)	
XX		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 7473.	
XX		

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128334P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135533P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.

PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 30-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145244P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 28-JUL-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149476P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151033P.
PR 31-AUG-1999; 99US-0151438P.

PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 36; DB 3; Length 257;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LGTYFDS 10
Db 10 LGLYFDT 17

RESULT 32

AAG48547
ID AAG48547 standard; protein; 257 AA.

XX AAG48547;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 61317.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

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Query Match 66.7%; Score 36; DB 3; Length 257;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYRFD 10
DB 10 LGTYRFD 17

RESULT 33
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ID ADN46472 standard; protein; 258 AA.

XX ADN46472;
AC
XX
DT 01-JUL-2004 (first entry)
XX
DE Thermococcus kodakarensis KOD1 protein sequence SegID50.

XX gene disruption; gene targeting; marker gene; transformation;
KW homologous recombination; hyperthermostable archaeobacterium; KOD1;
KW gene structure; gene function; enzyme activity; medicine;
KW forensic science; food; drug inspection; molecular biology; immunology.

XX Thermococcus kodakarensis.

XX
XX
PN WO2004022736-A1.

XX
XX
PD 18-MAR-2004.

XX
XX
PF 29-AUG-2003; 2003WO-IB003597.
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Query Match 66.7%; Score 36; DB 3; Length 260;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 36
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ID AAG48543 standard; protein; 354 AA.

AC AAG48543;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 61311.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX Arabidopsis thaliana.

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PN 06-SEP-2000.

PD 25-FEB-2000; 2000EP-00301439.

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Query Match 66.7%; Score 36; DB 3; Length 354;
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Qy 3 LGTYRFD 10
 Db 107 LGTYRFD 114

RESULT 37
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 ID ABB67540 standard; protein; 361 AA.
 XX ABB67540;
 AC ABB67540;
 XX 26-MAR-2002 (first entry)
 DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster polypeptide SEQ ID NO 29412.
 DE Drosophila melanogaster polypeptide SEQ ID NO 29412.
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX Drosophila melanogaster.
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US009231.
 PF 23-MAR-2001; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PMD, Myers EW;
 PI N-FSDB; ABL11643.
 DR WPI; 2001-656860/75.
 XX N-FSDB; ABL11643.
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signaling and cell-cell
 interactions.
 PS Disclosure; SEQ ID NO 29412; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 capable of detecting 1000 or more genes from Drosophila. The invention is
 useful in developmental biology and in elucidating cell signaling and
 cell-cell interactions in higher eukaryotes for the development of
 insecticides, therapeutics and pharmaceutical drugs. The invention
 discloses genomic DNA sequences (ABL16176-AB130511), expressed DNA
 sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 ABB72072). The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 361 AA;
 SQ

Query Match 66.7%; Score 36; DB 4; Length 361;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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 DB 21 LNTYRFD 28

RESULT 38

AAB75213
 ID AAB75213 standard; protein; 361 AA.

XX AAB75213;

DT 03-APR-2001 (first entry)

DE Drosophila gustatory receptor GR47A.1 protein sequence.

XX Gustatory receptor; fruit fly; taste; pheromone; semiochemical;

KM crop damage; pest control.

XX Drosophila melanogaster.

XX WO200077208-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016211.

XX 14-JUN-1999; 99US-0138668P.

PR 10-FEB-2000; 2000US-0181704P.

XX (UYVA) UNIV YALE.

PI Carlson PJ, Clyne PJ, Warr CG;

DR WPI; 2001-061873/07.

XX N-PSDB; AAF63752.

PS Claim 12; Page 146-147; 227pp; English.

XX This invention relates to polynucleotide sequences AAF63732 - AAF63777

CC which encode Drosophila gustatory receptor proteins represented by

CC sequences AAB75193 - AAB75238. The invention includes methods for

CC determining gustatory receptor ligands. Also included is a method for

CC modulating the expression of the DNA encoding the receptor. The DNA and

CC protein sequences may be used for the identification of compounds, e.g.

CC pheromones and other semiochemicals, which may be used for pest

CC management. The DNA sequences may also be used for behavioural studies

CC involving gustatory systems in various organisms. Also, the DNA sequences

CC may also be used to track down gustatory receptor genes in insects that

CC damage crops or transmit diseases

XX

RESULT 39

AAB30515
 ID AAB30515 standard; protein; 361 AA.

AC AAB30515;

XX 24-FEB-2003 (first entry)

DE Fruit fly gustatory receptor protein, Gr47A1.

XX Fruit fly; gustatory receptor; Gr; odorant receptor; Or; pesticide;

KM Gr47A1.

XX Drosophila melanogaster.

XX WO200266593-A2.

XX 06-SEP-2002.

XX 22-FEB-2002; 2002WO-US005414.

XX 23-FEB-2001; 2001US-0271319P.

XX (UYCO) UNIV COLUMBIA NEW YORK.

PI Axel R, Scott K;

DR WPI; 2002-698668/75.

XX Novel nucleic acid encoding insect gustatory or odorant receptor protein

XX useful for identifying a compound which specifically binds to the

XX receptor for controlling a pest population in an area.

XX Disclosure; Page 203-205; 264pp; English.

XX The invention relates to an isolated nucleic acid encoding an insect

XX gustatory receptor (Gr) or odorant receptor (Or) protein which comprises

XX seven transmembrane domains and a C-terminal domain comprising

XX consecutive amino acids. The invention is useful for identifying a

XX compound which activates the insect receptor or inhibits the activity of

XX the insect receptor. The purified insect receptor protein is embedded in

XX a lipid bilayer. The invention is sprayed for combating ingestion of

XX crops by pest insects, combating disease-carrying insects in an area and

XX controlling a pest population in an area. The invention is useful for

XX detecting the presence of insect gustatory or odorant receptor and for

XX inhibiting the function of the receptor in humans or animals or in

XX biological fluids isolated from them. The invention is also useful for

XX identifying or isolating other insect receptors and for combating pest

XX nuisances. The present sequence is fruit fly gustatory receptor (Gr)

XX protein

XX Sequence 361 AA;

XX Query Match 66.7%; Score 36; DB 5; Length 361;

XX Best Local Similarity 75.0%; Pred. No. 2.2e+02;

XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYRPS 10
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 DB 21 LNTYRFD 28

RESULT 40

ADB70112
 ID ADB70112 standard; protein; 387 AA.

XX ADB70112;

DT 04-DEC-2003 (first entry)

DE C. neoformans amino acid sequence SEQ ID NO:3156.

XX fungicide; gene therapy; infection.

XX Cryptococcus neoformans.

XX WO2003052076-A2.

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XX 26-JUN-2003.
PD
XX
XX 17-DEC-2002; 2002WO-US040225.
PF
XX
XX 17-DEC-2001; 2001US-0341261P.
PR
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Zamudio C, Eroshkin AM;
XX
XX WPI: 2003-533017/50.
DR N-PSDB; ADB69029.
XX
XX
XX PT New nucleic acid, useful for preparing a composition for treating an
XX PT infection caused by Cryptococcus neoformans.
XX
XX PS Claim 9; SEQ ID NO 3156; 136pp; English.
XX
XX CC The invention relates to a novel purified or isolated Cryptococcus
XX CC neoformans nucleic acid molecule comprising a sequence encoding a
XX CC polypeptide comprising a sequence not given in the specification. A
XX CC polynucleotide of the invention has fungicide activity, and may have a
XX CC use in gene therapy. The nucleic acid is useful for preparing a
XX CC composition for treating an infection caused by Cryptococcus neoformans.
XX CC The present sequence represents a C. neoformans sequence of the
XX CC invention. Note: The sequence data for this patent is not represented in
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
SQ Sequence 387 AA;

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Query Match 66.7%; Score 36; DB 7; Length 387;
Best Local Similarity 70.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 VKLGITYYFDS 10
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Db 24 IKLGTYLRDS 33

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 Job time : 32.3933 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Searched: 478139 seqs, 66318000 residues

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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4	54	100.0	130	4	US-09-764-304-18
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6	38	70.4	1278	4	US-09-604-957-3
7	37	68.5	94	4	US-09-543-681A-6788
8	37	68.5	137	4	US-09-107-532A-6082
9	37	68.5	388	3	US-09-134-001C-4951
10	37	68.5	685	4	US-09-489-039A-11090
11	35	64.8	118	2	US-08-379-057-30
12	35	64.8	226	4	US-09-710-279-1932
13	35	64.8	288	3	US-09-134-001C-4963
14	35	64.8	349	4	US-09-491-577-96
15	34	63.0	19	3	US-08-525-539A-41
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17	34	63.0	271	4	US-09-134-000C-4879
18	34	63.0	275	1	US-08-252-995D-13
19	34	63.0	275	2	US-08-834-108-13
20	34	63.0	319	4	US-09-107-532A-6410
21	34	63.0	365	4	US-09-134-000C-4931
22	34	63.0	373	4	US-09-248-796A-14832
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25	33	61.1	81	4	US-09-248-796A-19774
26	33	61.1	124	4	US-09-530-139-58
27	33	61.1	196	4	US-09-107-532A-5809

28	33	61.1	228	4	US-08-976-063E-14	Sequence 14, Appl
29	33	61.1	229	4	US-09-270-767-56999	Sequence 56999, A
30	33	61.1	265	4	US-09-248-796A-15824	Sequence 15824, A
31	33	61.1	357	4	US-09-248-796A-18015	Sequence 18015, A
32	33	61.1	368	4	US-09-489-039A-7783	Sequence 7783, Ap
33	33	61.1	549	4	US-09-543-681A-4720	Sequence 4720, Ap
34	33	61.1	766	4	US-09-328-352-8230	Sequence 8230, Ap
35	33	61.1	911	4	US-09-688-188B-92	Sequence 92, Appl
36	33	61.1	911	4	US-09-291-417D-92	Sequence 92, Appl
37	33	61.1	966	4	US-09-688-188B-154	Sequence 154, Appl
38	33	61.1	966	4	US-09-291-417D-154	Sequence 154, Appl
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40	32	59.3	264	4	US-09-107-532A-5034	Sequence 5034, Ap
41	32	59.3	273	4	US-09-328-352-6167	Sequence 6167, Ap
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ALIGNMENTS

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; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIMURA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-8

Query Match      100.0%; Score 54; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VKLGTYFDS 10
DB      109 VKLGTYFDS 118

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US-09-225-322B-18
; Sequence 18, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
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APPLICANT: HASEGAMA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHISHI
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/225,322B
CURRENT FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-18

Query Match 100.0%; Score 54; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
Db 109 VKLGYTFDS 118

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Sequence 8, Application US/09764304
Patent No. 6495666
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAMA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHISHI
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: cDNA KM-641
US-09-764-304-8

Query Match 100.0%; Score 54; DB 4; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
Db 109 VKLGYTFDS 118

RESULT 4
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Sequence 18, Application US/09764304
Patent No. 6495666
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAMA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHISHI
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: cDNA KM-641
US-09-764-304-18

Query Match 100.0%; Score 54; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
Db 109 VKLGYTFDS 118

RESULT 5
US-08-211-202-135
Sequence 135, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
APPLICANT: BAYER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSER: Borlun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-135

```

```

Query Match 77.8%; Score 42; DB 1; Length 120;
Best Local Similarity 87.5%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 LGTYFDS 10
DB 101 LGTYFDS 108

```

```

RESULT 6
US-09-604-957-3
Sequence 3, Application US/09604957
Patent No. 6486314
GENERAL INFORMATION:
APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 1278
TYPE: PRT
ORGANISM: Lactobacillus reuteri
US-09-604-957-3
Query Match 70.4%; Score 38; DB 4; Length 1278;

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Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTYFDS 10
DB 1221 GTYFDS 1227

```

```

RESULT 7
US-09-543-681A-6788
Sequence 6788, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETTON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709, 1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6788
LENGTH: 94
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-6788

```

```

Query Match 68.5%; Score 37; DB 4; Length 94;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 LGTYFDS 10
DB 21 LGTYFDS 28

```

```

RESULT 8
US-09-107-532A-6082
Sequence 6082, Application US/09107532A
Patent No. 6581275
GENERAL INFORMATION:
APPLICANT: LYNN A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

```

```

; INFORMATION FOR SEQ ID NO: 6082:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 137 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;       ORGANISM: Enterococcus faecium
;   FEATURE:
;       NAME/KEY: misc feature
;       LOCATION: (8) LOCATION 1..137
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6082:
US-09-107-532A-6082

Query Match
Best Local Similarity 68.5%; Score 37; DB 4; Length 137;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 KLGTYYFD 9
Db      124 KIGTYHD 131

RESULT 9
US-09-134-001C-4951
; Sequence 4951, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;   APPLICANT: Lynn Doucette-Stamm et al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;   FILE REFERENCE: GTC-007
;   CURRENT APPLICATION NUMBER: US/09/134,001C
;   CURRENT FILING DATE: 1998-08-13
;   PRIOR APPLICATION NUMBER: US 60/064,964
;   PRIOR FILING DATE: 1997-11-08
;   PRIOR APPLICATION NUMBER: US 60/055,779
;   PRIOR FILING DATE: 1997-08-14
;   NUMBER OF SEQ ID NOS: 5674
;   SEQ ID NO 4951
;   LENGTH: 388
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4951

Query Match
Best Local Similarity 68.5%; Score 37; DB 3; Length 388;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KLGTYYFDS 10
Db      250 RVGTYYFGS 258

RESULT 10
US-09-489-039A-11090
; Sequence 11090, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;   APPLICANT: Gary Breton et. al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;   FILE REFERENCE: 2709.2004001
;   CURRENT APPLICATION NUMBER: US/09/489,039A
;   CURRENT FILING DATE: 2000-01-27
;   PRIOR APPLICATION NUMBER: US 60/117,747
;   PRIOR FILING DATE: 1999-01-29
;   NUMBER OF SEQ ID NOS: 14342
;   SEQ ID NO 11090
;   LENGTH: 685
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
```

```

US-09-489-039A-11090

Query Match
Best Local Similarity 68.5%; Score 37; DB 4; Length 685;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 GTYYFDS 10
Db      577 GTYYFDS 583

RESULT 11
US-08-379-057-30
; Sequence 30, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
;   APPLICANT: Siadak, Anthony W.
;   APPLICANT: Hollenbaugh, Diane L.
;   APPLICANT: Gilliland, Lisa K.
;   APPLICANT: Gordon, Marcia L.
;   APPLICANT: Bajorath, Jürgen
;   APPLICANT: Aruffo, Alejandro A.
;   TITLE OF INVENTION: Monoclonal Antibodies Specific For
;   TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
;   TITLE OF INVENTION: In Diagnosis and Therapy
;   NUMBER OF SEQUENCES: 57
;   CORRESPONDENCE ADDRESSES:
;   ADDRESSER: Bristol-Myers Squibb Company
;   STREET: 3005 First Avenue
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98121
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: IBM PC compatible
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/379,057
;   FILING DATE: 26-JAN-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Poor, Brian W.
;   REGISTRATION NUMBER: 32,928
;   REFERENCE/DOCKET NUMBER: ONO133-
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 727-3670
;   TELEFAX: (206) 727-3601
;   INFORMATION FOR SEQ ID NO: 30:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 118 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FRAGMENT TYPE: internal
US-08-379-057-30

Query Match
Best Local Similarity 64.8%; Score 35; DB 2; Length 118;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TYVYFDS 10
Db      57 TYVYFDS 62

RESULT 12
US-09-710-279-1932
; Sequence 1932, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;   APPLICANT: KIMMERLY, WILLIAM JOHN
```

;/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;/ FILE REFERENCE: PU3480US
;/ CURRENT APPLICATION NUMBER: US/09/710,279
;/ CURRENT FILING DATE: 2000-11-09
;/ PRIOR APPLICATION NUMBER: 60/164,258
;/ PRIOR FILING DATE: 1999-11-09
;/ NUMBER OF SEQ ID NOS: 4472
;/ SOFTWARE: Patentin Ver. 2.1
;/ SEQ ID NO: 1932
;/ LENGTH: 226
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
;/ OTHER INFORMATION: amino acid sequence
US-09-710-279-1932

Query Match 64.8%; Score 35; DB 4; Length 226;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYFED 9
Db 211 KIGTYCFD 218

RESULT 13
US-09-134-001C-4963
;/ Sequence 4963, Application US/09134001C
;/ Patent No. 6380370
;/ GENERAL INFORMATION:
;/ APPLICANT: Lynn Doucelte-Stamm et al
;/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;/ TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;/ FILE REFERENCE: GTC-007
;/ CURRENT APPLICATION NUMBER: US/09/134,001C
;/ CURRENT FILING DATE: 1998-08-13
;/ PRIOR APPLICATION NUMBER: US 60/064,964
;/ PRIOR FILING DATE: 1997-11-08
;/ PRIOR APPLICATION NUMBER: US 60/055,779
;/ PRIOR FILING DATE: 1997-08-14
;/ NUMBER OF SEQ ID NOS: 5674
;/ SEQ ID NO: 4963
;/ LENGTH: 288
;/ TYPE: PRT
;/ ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4963

Query Match 64.8%; Score 35; DB 3; Length 288;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYFED 9
Db 273 KIGTYCFD 280

RESULT 14
US-09-491-577-96
;/ Sequence 96, Application US/09491577
;/ Patent No. 6610511
;/ GENERAL INFORMATION:
;/ APPLICANT: Yale University
;/ APPLICANT: Carlson, John R.
;/ APPLICANT: Kim, Hunhyong
;/ APPLICANT: Clyne, Peter J.
;/ APPLICANT: Marr, Coral G.
;/ TITLE OF INVENTION: No. 6610511el Family of Odorant Receptor Genes in Drosophila
;/ FILE REFERENCE: 44574-5061-US
;/ CURRENT APPLICATION NUMBER: US/09/491,577
;/ CURRENT FILING DATE: 2000-01-25
;/ EARLIER APPLICATION NUMBER: US 60/117,132
;/ EARLIER FILING DATE: 1999-01-25

;/ NUMBER OF SEQ ID NOS: 112
;/ SOFTWARE: Patentin Ver. 2.1
;/ SEQ ID NO: 96
;/ LENGTH: 349
;/ TYPE: PRT
;/ ORGANISM: Drosophila melanogaster
US-09-491-577-96

Query Match 64.8%; Score 35; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYYF 8
Db 61 LGTYYF 66

RESULT 15
US-08-525-539A-41
;/ Sequence 41, Application US/08525539A
;/ Patent No. 6309636
;/ GENERAL INFORMATION:
;/ APPLICANT: DO COUTO, FERNANDO J.R.
;/ APPLICANT: CERIANI, ROBERTO L.
;/ APPLICANT: PETERSON, JERRY A.
;/ TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
;/ TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
;/ TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
;/ NUMBER OF SEQUENCES: 81
;/ CORRESPONDENCE ADDRESSES:
;/ ADDRESSEE: MORRISON & FOERSTER
;/ STREET: 755 Page Mill Road
;/ CITY: Palo Alto
;/ STATE: CA
;/ COUNTRY: USA
;/ ZIP: 94304-1018
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patentin Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/525,539A
;/ FILING DATE: 14-SEP-1995
;/ CLASSIFICATION: 424
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: DYLAN, TYLER
;/ REGISTRATION NUMBER: 37,612
;/ REFERENCE/DOCKET NUMBER: 27633-20001.21
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 813-5600
;/ TELEFAX: (415) 494-0792
;/ TELEX: 706141
;/ INFORMATION FOR SEQ ID NO: 41:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 19 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
US-08-525-539A-41

Query Match 63.0%; Score 34; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LGTYYFDS 10
Db 8 LAVYYFDS 15

RESULT 16
US-07-942-245-22
;/ Sequence 22, Application US/07942245

Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Brian C.
TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-22

Query Match 63.0%; Score 34; DB 1; Length 115;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 LGTYFDS 10
DB 106 LAVYFDS 113
RESULT 17
US-09-134-000C-4879
Sequence 4879, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4879
LENGTH: 271
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4879

Query Match 63.0%; Score 34; DB 4; Length 271;
Best Local Similarity 62.5%; Pred. No. 1,2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 VKLGTYF 8

DB 47 IQLGTYF 54

RESULT 18
US-08-252-995D-13
Sequence 13, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kirdyck, Linda W
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-08-252-995D-13

Query Match 63.0%; Score 34; DB 1; Length 275;
Best Local Similarity 60.0%; Pred. No. 1,2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 VKLGTYFDS 10
DB 131 LKGNIFDS 140

RESULT 19
US-08-834-108-13
Sequence 13, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada

ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 516
ATTORNEY/AGENT INFORMATION:
NAME: Kirdyck, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-08-834-108-13

Query Match 63.0%; Score 34; DB 2; Length 275;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYFDS 10
Db 131 LKLGNTFFDS 140

RESULT 20
US-09-107-532A-6410
Sequence 6410, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277

INFORMATION FOR SEQ ID NO: 6410:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...319
SEQUENCE DESCRIPTION: SEQ ID NO: 6410:
US-09-107-532A-6410

Query Match 63.0%; Score 34; DB 4; Length 319;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10
Db 87 RLGTYYMET 95

RESULT 21
US-09-134-000C-4931
Sequence 4931, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patent version 3.1
SEQ ID NO 4931
LENGTH: 365
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4931

Query Match 63.0%; Score 34; DB 4; Length 365;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10
Db 115 RLGTYYLET 123

RESULT 22
US-09-248-796A-14832
Sequence 14832, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196,132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14832
LENGTH: 373
TYPE: PRT

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; ORGANISM: Candida albicans
US-09-248-796A-14832
Query Match
Best Local Similarity 63.0%; Score 34; DB 4; Length 373;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYVFD 10
DB 137 GSYVFDN 143

RESULT 23
US-09-543-681A-6460
; Sequence 6460, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709,1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6460
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6460

Query Match
Best Local Similarity 63.0%; Score 34; DB 4; Length 790;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYVFD 10
DB 708 VGATVFD 715

RESULT 24
US-09-248-796A-26385
; Sequence 26385, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196,132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26385
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26385

Query Match
Best Local Similarity 63.0%; Score 34; DB 4; Length 979;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LGTYVFD 10
DB 918 LGATVFD 925

RESULT 25
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US-09-248-796A-19774
; Sequence 19774, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196,132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19774
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19774

Query Match
Best Local Similarity 61.1%; Score 33; DB 4; Length 81;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYVFD 9
DB 17 IKMTVFD 25

RESULT 26
US-09-530-139-58
; Sequence 58, Application US/09530139
; Patent No. 6670453
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDERER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOOT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Anti-LAB-phage
US-09-530-139-58

Query Match
Best Local Similarity 61.1%; Score 33; DB 4; Length 124;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTYVFD 10
DB 57 GTYVFD 63

RESULT 27
US-09-107-532A-5809
; Sequence 5809, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
```


TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051,571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5809:
SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: mbac_feature
LOCATION: (B) LOCATION 1...196
SEQUENCE DESCRIPTION: SEQ ID NO: 5809:
US-09-107-532A-5809

Query Match 61.1%; Score 33; DB 4; Length 196;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYFPD 9
|||||
DB 65 GTTYFE 70

RESULT 28
US-08-976-063E-14
Sequence 14, Application US/08976063E
Patent No. 6524831
GENERAL INFORMATION:
APPLICANT: Steinhuchel, Alexander
APPLICANT: Pfeleert, Horst
APPLICANT: Rabenhorst, Jürgen
TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION OF CONIFERYL,
ALCOHOL, CONFERYLALDEHYDE, PERULIC ACID, VANILLIN AND
TITLE OF INVENTION: VANILLIC ACID AND THEIR USE
FILE REFERENCE: Bayer-9998-CAO
CURRENT APPLICATION NUMBER: US/08/976,063E
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 196 49 655.1 GERMANY
PRIOR FILING DATE: 1996-11-29
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentlin Ver. 2.1
SEQ ID NO 14

LENGTH: 228
TYPE: PRT
ORGANISM: not required under old rule
US-08-976-063E-14

Query Match 61.1%; Score 33; DB 4; Length 228;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFPD 9
|||||
DB 186 LGTYPAD 192

RESULT 29
US-09-270-767-56999
Sequence 56999, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentlin Ver. 2.0
SEQ ID NO 56999
LENGTH: 229
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-56999

Query Match 61.1%; Score 33; DB 4; Length 229;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYFP 8
:|||||
DB 97 LELGTYFP 104

RESULT 30
US-09-248-796A-15824
Sequence 15824, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15824
LENGTH: 265
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-15824

Query Match 61.1%; Score 33; DB 4; Length 265;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFPDS 10
:|||||
DB 68 VGATYFDS 75

RESULT 31

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US-09-248-796A-18015
; Sequence 18015, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18015
; LENGTH: 357
; TYPE: PRN
; ORGANISM: Candida albicans
US-09-248-796A-18015

Query Match
Best Local Similarity 61.1%; Score 33; DB 4; Length 357;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYFD 9
Db 265 KPSTYFD 272

RESULT 32
US-09-489-039A-7783
; Sequence 7783, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7783
; LENGTH: 368
; TYPE: PRN
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7783

Query Match
Best Local Similarity 61.1%; Score 33; DB 4; Length 368;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYFD 8
Db 305 QLGTYFD 311

RESULT 33
US-09-543-681A-4720
; Sequence 4720, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
```

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; SEQ ID NO 4720
; LENGTH: 549
; TYPE: PRN
; ORGANISM: Proteus mirabilis
US-09-543-681A-4720

Query Match
Best Local Similarity 61.1%; Score 33; DB 4; Length 549;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYFD 8
Db 301 QLGTYFD 307

RESULT 34
US-09-328-352-8230
; Sequence 8230, Application US/09328352
; Patent No. 6562938
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8230
; LENGTH: 766
; TYPE: PRN
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8230

Query Match
Best Local Similarity 61.1%; Score 33; DB 4; Length 766;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKGTY 7
Db 289 VKAGTY 295

RESULT 35
US-09-688-188B-92
; Sequence 92, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 911
; TYPE: PRN
; ORGANISM: Murine sp.
US-09-688-188B-92

Query Match
Best Local Similarity 61.1%; Score 33; DB 4; Length 911;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFD 9
Db 97 LGATYFD 103
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RESULT 36
US-09-291-417D-92
; Sequence 92, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 92
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-291-417D-92

Query Match 61.1%; Score 33; DB 4; Length 911;
Best Local Similarity 71.4%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYYPD 9
Db 97 LGATYYD 103

RESULT 37
US-09-688-188B-154
; Sequence 154, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 154
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-688-188B-154

Query Match 61.1%; Score 33; DB 4; Length 966;
Best Local Similarity 71.4%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYYPD 9
Db 97 LGATYYD 103

RESULT 38
US-09-291-417D-154
; Sequence 154, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO

; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 154
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-291-417D-154

Query Match 61.1%; Score 33; DB 4; Length 966;
Best Local Similarity 71.4%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYYPD 9
Db 97 LGATYYD 103

RESULT 39
US-09-270-767-32459
; Sequence 32459, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 32459
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32459

Query Match 59.3%; Score 32; DB 4; Length 180;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TYTFDS 10
Db 61 TYTFDN 66

RESULT 40
US-09-107-532A-5034
; Sequence 5034, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5034:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...264
; SEQUENCE DESCRIPTION: SEQ ID NO: 5034:
US-09-107-532A-5034

Query Match      59.3%; Score 32; DB 4; Length 264;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 KLGTYFFD 9
        |||:| ||
Db      96 KLGTYFFD 103
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Search completed: December 17, 2004, 18:32:08
Job time : 7.06742 secs

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OM protein - protein search, using ew model

Run on: December 17, 2004, 18:20:33 ; Search time 19.3258 Seconds
(without alignments)
185.159 Million cell updates/sec

Title: US-10-089-500-5

Perfect score: 54

Sequence: 1 VLDGTYRPS 10

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Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/ptodata/2/pubppa/US09B_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	54	100.0	130	14	US-10-265-713-8
4	54	100.0	130	14	US-10-265-713-8
5	54	100.0	130	14	US-10-166-626-8
6	54	100.0	130	14	US-10-166-626-8
7	40	74.1	446	17	US-10-739-930-10028
8	39	72.2	195	17	US-10-425-115-365506
9	39	72.2	206	17	US-10-425-115-204796
10	39	72.2	341	17	US-10-425-115-311275
11	39	72.2	424	17	US-10-425-115-204801
12	39	72.2	427	15	US-10-425-114-46787
13	39	72.2	435	16	US-10-437-963-139528

14	39	72.2	572	17	US-10-425-115-204798	Sequence 204798,
15	38	70.4	48	9	US-10-424-599-145556	Sequence 145556,
16	38	70.4	1781	15	US-09-995-749A-2	Sequence 2, Appl1
17	37	68.5	179	14	US-10-243-552-339	Sequence 339, App
18	37	68.5	380	11	US-09-833-245-1319	Sequence 1319, App
19	36	66.7	73	15	US-10-424-599-250992	Sequence 250992,
20	36	66.7	361	14	US-10-081-816-35	Sequence 35, Appl
21	36	66.7	361	15	US-10-447-328-42	Sequence 42, Appl
22	36	66.7	387	15	US-10-320-797-3156	Sequence 3156, Ap
23	36	66.7	433	14	US-10-369-493-11075	Sequence 11075, A
24	36	66.7	440	15	US-10-424-599-154451	Sequence 154451,
25	36	66.7	675	17	US-10-782-141-21	Sequence 2137, Ap
26	36	66.7	675	17	US-10-782-096-22	Sequence 3076, Ap
27	36	66.7	675	17	US-10-781-979-23	Sequence 2135, Ap
28	36	66.7	859	17	US-10-425-115-270359	Sequence 270359,
29	36	66.7	931	16	US-10-437-963-106243	Sequence 106243,
30	35	64.8	23	10	US-09-880-748-2132	Sequence 2132, Ap
31	35	64.8	23	10	US-09-880-748-3076	Sequence 3076, Ap
32	35	64.8	23	14	US-10-293-418-2132	Sequence 2135, Ap
33	35	64.8	23	14	US-10-293-418-2132	Sequence 3076, Ap
34	35	64.8	118	16	US-10-437-963-16875	Sequence 16875,
35	35	64.8	138	17	US-10-425-115-263537	Sequence 263537,
36	35	64.8	139	15	US-10-424-599-178546	Sequence 178546,
37	35	64.8	139	15	US-10-424-599-178546	Sequence 178546,
38	35	64.8	172	15	US-10-424-599-179462	Sequence 179462,
39	35	64.8	255	10	US-09-880-748-1054	Sequence 242803,
40	35	64.8	255	10	US-09-880-748-1054	Sequence 4, Appl1
41	35	64.8	255	10	US-09-880-748-1056	Sequence 1056, Ap
42	35	64.8	255	10	US-09-880-748-1065	Sequence 1065, Ap
43	35	64.8	255	10	US-09-880-748-1065	Sequence 1786, Ap
44	35	64.8	255	14	US-10-293-418-4	Sequence 4, Appl1
45	35	64.8	255	14	US-10-293-418-1054	Sequence 1054, Ap

ALIGNMENTS

RESULT 1
US-09-764-304-8
Sequence 8, Application US/09764304
Patent No. US2002026036X1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KURAMA, YOSHIEHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09764,304
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,660
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CDNA KM-641
US-09-764-304-8

Query Match 100.0%; Score 54; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
Db 109 VKLGYTFDS 118

RESULT 2

US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER FILING DATE: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA KM-641
US-09-764-304-18

Query Match 100.0%; Score 54; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
Db 109 VKLGYTFDS 118

RESULT 3

US-10-265-713-8
; Sequence 8, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133

; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-265-713-8

RESULT 4

US-10-265-713-18
; Sequence 18, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-265-713-18

QY 1 VKLGYTFDS 10
Db 109 VKLGYTFDS 118

RESULT 5

US-10-166-626-8
; Sequence 5
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-265-713-18

Query Match 100.0%; Score 54; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
Db 109 VKLGYTFDS 118

RESULT 5
US-10-166-626-8

Sequence 8, Application US/10166626
Publication No. US20030166876A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/166,626
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-166-626-8

Query Match 100.0%; Score 54; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYFDS 10
DB 109 VKLGTYFDS 118

RESULT 6
US-10-166-626-18
Sequence 18, Application US/10166626
Publication No. US20030166876A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/166,626
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 130

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-166-626-18

Query Match 100.0%; Score 54; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYFDS 10
DB 109 VKLGTYFDS 118

RESULT 7
US-10-739-930-10028
Sequence 10028, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: KOVALIC, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 10028
LENGTH: 446
TYPE: PRT
ORGANISM: Trilicium aestivum
FEATURE:
OTHER INFORMATION: Clone ID: TRIAE-23APR03-C244_147.p
US-10-739-930-10028

Query Match 74.1%; Score 40; DB 17; Length 446;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYFDS 10
DB 195 VILGQYFDS 204

RESULT 8
US-10-425-115-365506
Sequence 365506, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J.
APPLICANT: KOVALIC, David K.
APPLICANT: ZHOU, Yihua
APPLICANT: CAO, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 365506
LENGTH: 195
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1).(195)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_96506C.1.p
US-10-425-115-365506

Query Match 72.2%; Score 39; DB 17; Length 195;
Best Local Similarity 87.5%; Pred. No. 76;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
|||
Db 145 LGQYFDS 152

RESULT 9
US-10-425-115-204796
; Sequence 204796, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 204796
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(206)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_118363C.1.pep
US-10-425-115-204796

Query Match 72.2%; Score 39; DB 17; Length 206;
Best Local Similarity 87.5%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
|||
Db 169 LGQYFDS 176

RESULT 10
US-10-425-115-311275
; Sequence 311275, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 311275
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_46938C.1.pep
US-10-425-115-311275

Query Match 72.2%; Score 39; DB 17; Length 341;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
|||
Db 159 LGQYFDS 166

RESULT 11
US-10-425-115-204801
; Sequence 204801, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 204801
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(424)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_118368C.1.pep
US-10-425-115-204801

Query Match 72.2%; Score 39; DB 17; Length 424;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
|||
Db 150 LGQYFDS 157

RESULT 12
US-10-425-114-46787
; Sequence 46787, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46787
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700799057_FLI.pep
US-10-425-114-46787

Query Match 72.2%; Score 39; DB 15; Length 427;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
|||
Db 150 LGQYFDS 157

RESULT 13

US-10-437-963-139528
; Sequence 139528, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 139528
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_40810C.1.pap
US-10-437-963-139528

Query Match
Best Local Similarity 72.2%; Score 39; DB 16; Length 435;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
Db 146 LGQYFDS 153

RESULT 14
US-10-425-115-204798
; Sequence 204798, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 204798
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) (572)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_118365C.1.pap
US-10-425-115-204798

Query Match
Best Local Similarity 72.2%; Score 39; DB 17; Length 572;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
Db 355 LGQYFDS 362

RESULT 15
US-10-424-599-145556

; Sequence 145556, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145556
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102456C.1.pap
US-10-424-599-145556

Query Match
Best Local Similarity 70.4%; Score 38; DB 15; Length 48;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLQTYFDS 9
Db 12 KLQTYFDS 19

RESULT 16
US-09-995-749A-2
; Sequence 2, Application US/09995749A
; Patent No. US20020155568A1
; GENERAL INFORMATION:
; APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
; APPLICANT: DIJKHUIZEN, LUBBERT
; APPLICANT: RAHACUI, HAKIM
; APPLICANT: LEER, ROBERT-JAN
; TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
; FILE REFERENCE: B043388-CIP
; CURRENT APPLICATION NUMBER: US/09/995, 749A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 09/604, 957
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: EPO 00201871.1
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1781
; TYPE: PRT
; ORGANISM: Lactobacillus reuteri
US-09-995-749A-2

Query Match
Best Local Similarity 70.4%; Score 38; DB 9; Length 1781;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYFDS 10
Db 1724 GTYFDS 1730

RESULT 17
US-10-243-552-339
; Sequence 339, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi

APPLICANT: Ma, Yungqing
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 807A
CURRENT APPLICATION NUMBER: US/10/243,552
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/322,511
PRIOR FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/04927
PRIOR FILING DATE: 2001-02-26
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 998
SOFTWARE: PL_FL_genes Version 5.0
SEQ ID NO 339
LENGTH: 179
TYPE: PRT
ORGANISM: Homo sapiens
US-10-243-552-339

Query Match 68.5%; Score 37; DB 14; Length 179;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
DB 150 LGTYFDS 157

RESULT 18
US-09-833-245-1319
Sequence 1319, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PFS46PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1319
LENGTH: 380
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-1319

Query Match 68.5%; Score 37; DB 11; Length 380;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10

DB 183 LGTYFDS 190

RESULT 19
US-10-424-599-250992
Sequence 250992, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 250992
LENGTH: 73
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_68675C.1.pep
US-10-424-599-250992

Query Match 66.7%; Score 36; DB 15; Length 73;
Best Local Similarity 60.0%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VKLGTYFDS 10
DB 42 IYFSTYFDS 51

RESULT 20
US-10-081-816-35
Sequence 35, Application US/10081816
Publication No. US20030045472A1
GENERAL INFORMATION:
APPLICANT: Axel, Richard
APPLICANT: Scott, Kristin
TITLE OF INVENTION: Chemosensory Gene Family Encoding Gustatory And Olfactory Receptor
FILE REFERENCE: 0575/64019-A/JPM/ADM
CURRENT APPLICATION NUMBER: US/10/081,816
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/271,319
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 361
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-10-081-816-35

Query Match 66.7%; Score 36; DB 14; Length 361;
Best Local Similarity 75.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
DB 21 LNTYFDT 28

RESULT 21
US-10-447-328-42
Sequence 42, Application US/10447328
Publication No. US20040003419A1
GENERAL INFORMATION:
APPLICANT: Carlson, John R.

APPLICANT: Clyne, Peter J.
APPLICANT: Warr, Coral G.
APPLICANT: Yale University
TITLE OF INVENTION: No. US20040003419A1el Taste Receptors in Drosophila
FILE REFERENCE: 44574-5072
CURRENT APPLICATION NUMBER: US/10/447,328
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: US/09/593,519
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/138,668
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 60/181,704
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 361
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-10-447-328-42

Query Match 66.7%; Score 36; DB 15; Length 361;
Best Local Similarity 75.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
DB 21 LNTYFDT 28

RESULT 22
US-10-320-797-3156
Sequence 3156, Application US/10320797
Publication No. US20040014955A1
GENERAL INFORMATION:
APPLICANT: Eroshkin, Alexey M.
APPLICANT: Zamudio, Carlos
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
FILE REFERENCE: 10182-021-999
CURRENT APPLICATION NUMBER: US/10/320,797
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: 60/341,261
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 3361
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3156
LENGTH: 387
TYPE: PRT
ORGANISM: Cryptococcus neoformans
US-10-320-797-3156

Query Match 66.7%; Score 36; DB 15; Length 387;
Best Local Similarity 70.0%; Pred. No. 4.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGYFDS 10
DB 24 IKLGLYRDS 33

RESULT 23
US-10-369-493-11075
Sequence 11075, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11075
LENGTH: 433
TYPE: PRT
ORGANISM: Periplasma acidarmanus
US-10-369-493-11075

Query Match 66.7%; Score 36; DB 14; Length 433;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 XLGTYFDS 10
DB 136 KIGTYWYDS 144

RESULT 24
US-10-424-599-154451
Sequence 154451, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yinhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 154451
LENGTH: 440
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(440)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_110491C.1.pcp
US-10-424-599-154451

Query Match 66.7%; Score 36; DB 15; Length 440;
Best Local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
DB 154 LGQYFDT 161

RESULT 25
US-10-782-141-21
Sequence 21, Application US/10782141
Publication No. US20040197917A1
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Hargies, Tracy
APPLICANT: Koziele, Michael G.
APPLICANT: Duck, Nicholas B.
APPLICANT: Carr, Brian
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274143
CURRENT APPLICATION NUMBER: US/10/782,141
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/448,632

; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-21

Query Match 66.7%; Score 36; DB 17; Length 675;
Best Local Similarity 85.7%; Pred. No. 8.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTYFDS 10
Db 627 GNYFDS 633

RESULT 26
US-10-782-096-22
; Sequence 22, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10/782,096
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,633
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-096-22

Query Match 66.7%; Score 36; DB 17; Length 675;
Best Local Similarity 85.7%; Pred. No. 8.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTYFDS 10
Db 627 GNYFDS 633

RESULT 27
US-10-781-979-23
; Sequence 23, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 675

; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-23

Query Match 66.7%; Score 36; DB 17; Length 675;
Best Local Similarity 85.7%; Pred. No. 8.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTYFDS 10
Db 627 GNYFDS 633

RESULT 28
US-10-425-115-270359
; Sequence 270359, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 270359
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_178164C.1.pcp
US-10-425-115-270359

Query Match 66.7%; Score 36; DB 17; Length 859;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYFDS 10
Db 430 GNYFDS 436

RESULT 29
US-10-437-963-106243
; Sequence 106243, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106243
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(931)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_10705C.1.pep
US-10-437-963-106243

Query Match
Best Local Similarity 66.7%; Score 36; DB 16; Length 931;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTYFDS 10
: : : : :
Db 471 GTHYFDS 477

RESULT 30

US-09-880-748-2132
; Sequence 2132, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2132
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2132

Query Match
Best Local Similarity 64.8%; Score 35; DB 10; Length 23;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9
: : : : :
Db 14 INVGPYYFD 22

RESULT 31

US-09-880-748-3076
; Sequence 3076, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3076
; LENGTH: 23

TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-3076

Query Match
Best Local Similarity 64.8%; Score 35; DB 10; Length 23;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9
: : : : :
Db 14 INVGPYYFD 22

RESULT 32

US-10-293-418-2132
; Sequence 2132, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2132
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2132

Query Match
Best Local Similarity 64.8%; Score 35; DB 14; Length 23;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9
: : : : :
Db 14 INVGPYYFD 22

RESULT 33

US-10-293-418-3076
; Sequence 3076, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25

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/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-16
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3076
/ LENGTH: 23
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-418-3076

Query Match      64.8%; Score 35; DB 14; Length 23;
Best Local Similarity 55.6%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 2; Gaps 0; Indels 0;
```

QY 1 VKLGYTFD 9
DB 14 INVGYTFD 22

```
RESULT 34
US-10-437-963-168775
/ Sequence 168775, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazov, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 168775
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(118)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_67257C.1.pep
US-10-437-963-168775

Query Match      64.8%; Score 35; DB 16; Length 118;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 2; Gaps 0; Indels 0;
```

QY 1 VKLGYTFD 10
DB 42 VGVSTYTFD 51

```
RESULT 35
US-10-425-115-263537
/ Sequence 263537, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
```

```
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 263537
/ LENGTH: 138
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(138)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_171959C.1.pep
US-10-425-115-263537

Query Match      64.8%; Score 35; DB 17; Length 138;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Gaps 0; Indels 0;
```

QY 1 VKLGYTFD 10
DB 107 VNLGYTFSS 116

```
RESULT 36
US-10-424-599-178546
/ Sequence 178546, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Zhou, Yihua
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 178546
/ LENGTH: 139
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_132244C.1.pep
US-10-424-599-178546

Query Match      64.8%; Score 35; DB 15; Length 139;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 2; Gaps 0; Indels 0;
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QY 1 VKLGYTFD 10
DB 42 VAVGYTFD 51

```
RESULT 37
US-10-424-599-179462
/ Sequence 179462, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Zhou, Yihua
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 179462
LENGTH: 139
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_133070C.1.pep
US-10-424-599-179462

Query Match 64.8%; Score 35; DB 15; Length 139;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYDFDS 10
DB 100 LGTYDFDS 107

RESULT 38
US-10-424-599-242803
Sequence 242803, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 242803
LENGTH: 172
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_61280C.1.pep
US-10-424-599-242803

Query Match 64.8%; Score 35; DB 15; Length 172;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYDFDS 10
DB 57 LGTYDFDS 64

RESULT 39
US-09-880-748-4
Sequence 4, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4

LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-4

Query Match 64.8%; Score 35; DB 10; Length 255;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYFPD 9
DB 112 INVGPYFPD 120

RESULT 40
US-09-880-748-1054
Sequence 1054, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1054
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1054

Query Match 64.8%; Score 35; DB 10; Length 255;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYFPD 9
DB 112 INVGPYFPD 120

Search completed: December 17, 2004, 18:37:59
Job time : 20.3258 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:11:22 / Search time 3.93258 Seconds
(without alignments)
244.665 Million cell updates/sec

Title: US-10-089-500-5

Perfect score: 54

Sequence: 1 VKLGTYFDS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	79.6	456	2 D97168	uncharacterized pro
2	40	74.1	144	2 B41287	Ig heavy chain pre
3	39	72.2	2817	2 B97033	uncharacterized pr
4	38	70.4	587	1 B44276	coat protein VP1 -
5	38	70.4	716	1 VCPV2M	coat protein VP1 -
6	38	70.4	718	1 VCPVIM	coat protein VP1 -
7	38	70.4	847	2 S75975	hypothetical prote
8	38	70.4	907	2 A86460	99.9K hypothetical
9	38	70.4	921	2 S49965	probable membrane
10	37	68.5	814	2 T02130	hypothetical prote
11	36	66.7	203	2 C69872	hypothetical prote
12	36	66.7	361	2 T48029	hypothetical prote
13	36	66.7	637	2 P90257	hypothetical prote
14	35	64.8	222	2 T31541	hypothetical prote
15	35	64.8	228	2 S09772	hypothetical prote
16	35	64.8	271	2 E72331	hypothetical prote
17	35	64.8	339	2 T21476	hypothetical prote
18	35	64.8	372	2 C86650	endo-1,4-beta-xyla
19	35	64.8	669	2 T28028	hypothetical prote
20	35	64.8	685	2 T22223	sel-1 protein - Ca
21	35	64.8	696	2 G88851	protein ZK629.10
22	35	64.8	837	2 B89583	protein K07E3.2
23	35	64.8	1113	2 T20140	hypothetical prote
24	34	63.0	84	2 A46158	nicotinic acetylch
25	34	63.0	110	2 A32189	Ig heavy chain V r
26	34	63.0	110	2 S09631	hypothetical prote
27	34	63.0	140	2 PH1486	Ig heavy chain V r
28	34	63.0	140	2 PH1499	Ig heavy chain V r
29	34	63.0	204	2 B90868	hypothetical prote

30	34	63.0	209	2 C70424	hypothetical prote
31	34	63.0	230	2 D85750	hypothetical prote
32	34	63.0	258	2 B81307	thiamin biosynthes
33	34	63.0	277	2 A64659	outer membrane pro
34	34	63.0	277	2 B71856	probable outer mem
35	34	63.0	309	2 T08150	chitinase (EC 3.2.
36	34	63.0	357	2 T48055	hypothetical prote
37	34	63.0	510	2 C64883	membrane protein Y
38	34	63.0	524	2 A45472	protein kinase (EC
39	34	63.0	586	2 F64186	ABC-type transport
40	34	63.0	627	2 AD1818	N-acetylglucosyl-L
41	34	63.0	692	2 G90284	hypothetical prote
42	34	63.0	705	2 A48144	protein kinase CDC
43	34	63.0	784	2 A10513	organic solvent to
44	34	63.0	1411	2 A84460	probable retroelem
45	34	63.0	1943	2 B64596	toxin-like outer m

ALIGNMENTS

RESULT 1

D97168
uncharacterized protein, CCEB homolog [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: D97168
R/Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.U.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: D97168
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-456 <KUR>
A/Cross-references: UNIPROT:Q97H36; GB:AE001437; P1DN:AAK80135.1; P1D:G15025172; GSPDB:G15025172
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetic: CAC2177

Query Match 79.6%; Score 43; DB 2; Length 456;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYFDS 10
DB 380 IKENTYFDS 389

RESULT 2

E41287
Ig heavy chain precursor V-V region (257-D) (anti-HIV-1) - human
C/Species: Homo sapiens (man)
C/Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Jan-2000
C/Accession: E41287
R/Andrie, J.S.; Johnson, S.; Zolla-Pazner, S.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 88, 7783-7787, 1991
A/Title: Molecular characterization of five human anti-human immunodeficiency virus type
A/Reference number: A41287; MUID:91352074; PMID:1909030
A/Accession: E41287
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-144 <AND>
A/Cross-references: GB:M67504; NID:G185413; P1DN:AA52946.1; P1D:G185414
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 144;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 KLGTYFPD 9
Db      117 RLGTYYDD 124

RESULT 3
B97033
uncharacterized protein, related to enterotoxins of other Clostridiales [imported] - C1C
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: B97033
R/Molling, J.; Breton, G.; Omelchenko, M.V.; Markanova, K.S.; Zeng, Q.; Gibson, R.; Lee,
., Daly, M.J.; Benmett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: B97033
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-2817 <KUR>
A/Cross-references: UNIPROT:Q97K42; GB:AE001437; PIDN:AK79053.1; PID:G15023993; GSPDB:C
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC1079

Query Match      72.4%; Score 39; DB 2; Length 2817;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VKLGYTFPDS 10
Db      612 IKGNTYFPDS 621

RESULT 4
B44276
coat protein VP1 - parvovirus luIII
C/Species: parvovirus luIII
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: B44276
R/Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
Virology 192, 339-345, 1993
A/Title: The complete nucleotide sequence of parvovirus luIII and localization of a unique
A/Reference number: A44276; MUID:93297126; PMID:8517025
A/Accession: B44276
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-587 <DIF>
A/Cross-references: UNIPROT:P36310; GB:M81888
C/Superfamily: parvovirus coat protein
C/Keywords: coat protein; glycoprotein
F/49,90,220,304,371,503,511,514,539,571/Binding site: carbohydrate (Asn) (covalent) #str

Query Match      70.4%; Score 38; DB 1; Length 587;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GTYTFPDS 10
Db      267 GTTYFPDT 273

RESULT 5
VCPV2M
coat protein VP1 - minute virus of mice
C/Species: minute virus of mice, murine parvovirus
C/Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C/Accession: A03700
R/Abstell, C.R.; Thomson, M.; Merchinsky, M.; Ward, D.C.
Nucleic Acids Res. 11, 999-1018, 1983
A/Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A/Reference number: A03696; MUID:83143341; PMID:6298737
A/Accession: A03700
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A/Molecule type: DNA
A/Residues: 1-716 <AST>
A/Cross-references: UNIPROT:P03137; EMBL:V01115
C/Superfamily: parvovirus coat protein
C/Keywords: coat protein

Query Match      70.4%; Score 38; DB 1; Length 716;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GTYTFPDS 10
Db      397 GTTYFPDT 403

RESULT 6
VCPV1M
coat protein VP1 - minute virus of mice (strain WVM1)
C/Species: minute virus of mice, murine parvovirus
C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C/Accession: B23008; B29510
R/Sahli, R.; McMaster, G.K.; Hart, B.
Nucleic Acids Res. 13, 3617-3633, 1985
A/Title: DNA sequence comparison between two tissue-specific variants of the autonomous f
A/Reference number: A23008; MUID:85212059; PMID:3855242
A/Accession: B23008
A/Molecule type: DNA
A/Residues: 1-718 <SAH>
A/Cross-references: UNIPROT:P07302; EMBL:X02481; NID:G60918; PIDN:CAB46507.1; PID:G541992
R/Abstell, C.R.; Gardiner, E.M.; Tattersall, P.
U. Virol. 57, 656-669, 1986
A/Title: DNA sequence of the lymphotropic variant of minute virus of mice, WVM(1), and c
A/Reference number: A29510; MUID:86115415; PMID:3502703
A/Accession: B29510
A/Molecule type: DNA
A/Residues: 1-143 'A', 145-718 <AST>
A/Cross-references: EMBL:M12032
C/Superfamily: parvovirus coat protein
C/Keywords: coat protein

Query Match      70.4%; Score 38; DB 1; Length 718;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GTYTFPDS 10
Db      399 GTTYFPDT 405

RESULT 7
S75975
hypotheetical protein - Synechocystis sp. (strain PCC 6803)
C/Species: Synechocystis sp.
C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S75975
R/Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S.
A/Reference number: S74322; MUID:97061201; PMID:8905231
A/Accession: S75975
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1847 <KAN>
A/Cross-references: UNIPROT:Q55476; EMBL:D64006; GB:AB001339; NID:G1001291; PIDN:BA10822
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C/Genetics:
A/Start codon: GTG

Query Match      70.4%; Score 38; DB 2; Length 847;
Best Local Similarity 66.7%; Pred. No. 47;
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Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 VKLGYTFD 9
|:|:|:|
Db 759 VNMGTTFD 767

RESULT 8
99.9K hypothetical protein T1B4.10 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86460
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Hughes, M.K.; Conaway, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huitzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maizel, R.; Marshall, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86460
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-907 <STO>
A:Cross-references: UNIPROT:Q9FM49; GB:AE005172; NID:g10998940; PIDN:AA626079.1; GSPDB:G69872
A:Map position: 1

Query Match
Best Local Similarity 70.4%; Score 38; DB 2; Length 907;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTYTDFDS 10
|:|:|:|
Db 795 GTTYTDFDS 801

RESULT 9
549965
probable membrane protein Y1L017C - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein Y13299.14C
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
R:Skellton, J.; Churcher, C.
submitted to the EMBL Data Library, December 1994
A:Reference number: S49951
A:Accession: S49965
A:Molecule type: DNA
A:Residues: 1-921 <SKE>
A:Cross-references: UNIPROT:P40547; EMBL:Z46881; NID:g599967; PID:g599982; GSPDB:GN00009
C:Genetics:
A:Gene: SGD:Y1L017C
A:Cross-references: SGD:S0001279
A:Map position: 9L
C:Superfamily: Saccharomyces cerevisiae probable membrane protein Y1L017C
C:Keywords: transmembrane protein
F:145-161/Domain: transmembrane #status predicted <TM1>
F:532-548/Domain: transmembrane #status predicted <TM2>

Query Match
Best Local Similarity 70.4%; Score 38; DB 2; Length 921;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LGTYTFD 9
|:|:|:|
Db 72 VGTYTFD 78

RESULT 10
T02130
hypothetical protein F8K4.5 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02130
R:Vysotskaya, V.S.; Schwartz, J.R.; Tortum, M.; Kwan, A.; Yu, G.; Oji, O.; Liu, S.; Li, R.; Rytz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.
A:Reference number: Z14574
A:Accession: T02130
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-814 <YVS>
A:Cross-references: UNIPROT:O80692; EMBL:AC004392; NID:g3282170; PID:g3367532; GSPDB:GN00009
A:Gene: ATSP:F8K4.5
A:Map position: 1

Query Match
Best Local Similarity 68.5%; Score 37; DB 2; Length 814;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VKLGYTFDS 10
|:|:|:|
Db 758 VKLGYTFDS 767

RESULT 11
C69872
hypothetical protein ylaE - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: C69872
R:Funet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bererck C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Enrich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrar, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritzt, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier ieh, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulo, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauer, P.; Laubert, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maubaud, S.; Maueel, Y.; M.; Ogawa, K.; Ogilwa, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portetelle, R.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, A.; Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serox, A.; Whiter, M.; Yamakoshi, A.; Tanaka, T.; Teperera, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Whiter, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C69872
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <KUN>
A:Cross-references: UNIPROT:O07629; GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13348.3
C:Genetics:
A:Gene: ylaE
A:Experimental source: strain 168

C:Superfamily: Bacillus subtilis hypothetical protein ylaE

Query Match
Best Local Similarity 66.7%; Score 36; DB 2; Length 203;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GTYTDFDS 10
|:|:|:|
Db 68 GTYTDFDS 74

RESULT 12
T48029
hypothetical protein T12C14.70 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48029
R:Barques, M.; Perez-Perez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; Mewes, H.W.; Ru
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24463
A:Accession: T48029
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361 <BAR>
A:Cross-references: UNIPROT:Q9LZ03; EMBL:AL162507
A:Experimental source: cultivar Columbia; BAC clone T12C14
C:Genetics:
A:Map position: 3
A:introns: 85/3; 108/2; 130/3; 182/2; 206/1; 229/1; 262/3
C:Date: T12C14.70
C:Superfamily: Arabidopsis thaliana hypothetical protein T12C14.70

Query Match 66.7%; Score 36; DB 2; Length 361;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VKLGTFFD 9
DB 242 KKGTTFE 249

RESULT 13
P90257
hypothetical protein SSO1053 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: F90257
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Coost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: F90257
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-637 <KUR>
A:Cross-references: UNIPROT:Q97Z76; GB:AE006641; NID:G13814241; PIDN:AAK41317.1; GSPDB:G
C:Genetics:
A:Gene: SSO1053

Query Match 66.7%; Score 36; DB 2; Length 637;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTFFD 9
DB 360 VKGNYYID 368

RESULT 14
T31541
hypothetical protein Y47D3A.9 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31541
R:Matthew, L.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21043
A:Accession: T31541
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-222 <TIL>
A:Cross-references: EMBL:AL117202; PIDN:CAB57890.1; CESP:Y47D3A.9
A:Experimental source: clone Y47D3A
C:Genetics:
A:Gene: CESP:Y47D3A.9

A:Note: intron positions not resolved (incomplete sequence)

Query Match 64.8%; Score 35; DB 2; Length 222;
Best Local Similarity 55.6%; Pred. No. 45;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTFFD 9
DB 110 IKHYYFE 118

RESULT 15
S09772
hypothetical protein U19 precursor - human cytomegalovirus (strain AD169)
C:Species: human cytomegalovirus, human herpesvirus 5
A:Note: host Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S09772
R:Chen, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; I
M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A:Reference number: S09749; MUID:90269039; PMID:2161319
A:Accession: S09772
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-228 <CHE>
A:Cross-references: UNIPROT:P16745; EMBL:X17403; NID:G59591; PIDN:CAA35442.1; PID:G59614
A:Note: this sequence was submitted to the EMBL Data Library, December 1989
C:Keywords: glycoprotein; transmembrane protein
F:/25/Domains: signal sequence #status predicted <SIG>
F:/6-228/Product: hypothetical protein U19 #status predicted <MAT>
F:/187-207/Domains: transmembrane #status predicted <TM>
F:/41,93,100,128,164/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 64.8%; Score 35; DB 2; Length 228;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTYFFDS 10
DB 107 GTYFFDS 113

RESULT 16
E72331
hypothetical protein TW0812 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: E72331
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: E72331
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-271 <ARN>
A:Cross-references: UNIPROT:Q9WZ93; GB:AE001748; GB:AE000512; NID:G4981332; PIDN:AAD35894
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TW0812
C:Superfamily: maltose transport protein malG

Query Match 64.8%; Score 35; DB 2; Length 271;
Best Local Similarity 60.0%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTFFDS 10
DB 62 VKLGNYYLNT 71

RESULT 17

T21476
 hypothetical protein F28C12.4 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T21476
 R/Kershaw, J.
 submitted to the EMBL Data Library, March 1997
 A/Reference number: Z19428
 A/Accession: T21476
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-339 <WIL>
 A/Cross-references: UNIPROT:O17844; EMBL:Z93380; PDB:CA807600.1; GSPDB:GN00019; CESP:F2
 A/Experimental source: clone F28C12
 C/Genetics:
 A/Map position: 1
 A/Introns: 85/3; 134/2; 224/2; 289/3
 C/Suprafamily: Caenorhabditis elegans hypothetical protein F18C5.1

Query Match 64.8%; Score 35; DB 2; Length 339;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYYP 8
 :|||:
 Db 164 LGTYYP 169

RESULT 18

C86660
 endo-1,4-beta-xylanase D [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C/Species: Lactococcus lactis subsp. lactis
 C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C/Accession: C86660
 R/Bolotin, A.; Winker, P.; Mauger, S.; Jalllon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s8
 A/Reference number: A86625; MUID:2125186; PMID:11337471
 A/Accession: C86660
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-372 <STO>
 A/Cross-references: UNIPROT:Q9C1S3; GB:AE005176; PID:g12723145; PDB:AAK04381.1; GSPDB:G
 A/Experimental source: strain IL1403
 C/Genetics:
 A/Map position: 5
 A/Introns: 41/1; 90/2; 210/3; 411/1; 548/1

Query Match 64.8%; Score 35; DB 2; Length 372;
 Best Local Similarity 71.4%; Pred. No. 75;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYYP 9
 :|||:
 Db 32 VGTYYP 38

RESULT 19

T28028
 hypothetical protein ZK829.10 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T28028
 R/Harris, B.
 submitted to the EMBL Data Library, May 1996
 A/Reference number: Z20458
 A/Accession: T28028
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-669 <WIL>

A/Cross-references: UNIPROT:O18300; EMBL:Z73899; PDB:CAA98079.2; GSPDB:GN00022; CESP:ZK8
 A/Experimental source: clone ZK829
 C/Genetics:
 A/Map position: 4
 A/Introns: 20/3; 146/1; 175/2; 222/3; 299/3; 344/1; 427/3; 526/3; 561/3; 595/3; 66

Query Match 64.8%; Score 35; DB 2; Length 669;
 Best Local Similarity 55.6%; Pred. No. 1.3e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYP 9
 :|||:
 Db 399 IKKTYYP 407

RESULT 20

T22223
 sel-1 protein - Caenorhabditis elegans
 N/Alternate names: regulator of lin-12
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T22223; S68303; S68304
 R/White, S.
 submitted to the EMBL Data Library, August 1996
 A/Reference number: Z19532
 A/Accession: T22223

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-685 <WIL>

A/Cross-references: UNIPROT:Q20423; EMBL:Z78063; PDB:CA801505.1; GSPDB:GN00023; CESP:F4
 A/Experimental source: clone F45D3
 R/Grant, B.; Greenwald, I.

Genetics 143, 237-247, 1996
 A/Title: The Caenorhabditis elegans sel-1 gene, a negative regulator of lin-12 and glp-1,
 A/Reference number: S68303; MUID:96304591; PMID:8722778
 A/Accession: S68303

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-685 <GRA>

A/Cross-references: GB:U50828; NID:g1255198; PDB:AA47112.1; PID:g1255199
 A/Accession: S68304
 A/Status: preliminary

A/Molecule type: mRNA
 A/Residues: 1-685 <GR2>
 A/Cross-references: EMBL:U50829; NID:g1255200; PID:g1255201
 C/Genetics:
 A/Map position: 5

Query Match 64.8%; Score 35; DB 2; Length 685;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYP 8
 :|||:
 Db 554 VKLGTYYP 561

RESULT 21

G88851
 protein ZK829.10 [imported] - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C/Accession: G88851
 R/anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
 A/Reference number: A75000; MUID:99069613; PMID:9851916
 A/Note: see webites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
 A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A/Accession: G88851

A:Cross-references: UNIPROT:P16748; EMBL:X17403; NID:G59591; PIDN:CAA35383.1; PID:G18139
A>Note: this sequence was submitted to the EMBL Data Library, December 1989
C:Superfamily: human cytomegalovirus hypothetical protein UM68

Query Match 63.0%; Score 34; DB 2; Length 110;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYFDS 10
DB 63 IELGVFFSS 72

RESULT 27

PH1486
ig heavy chain V region (clone X7-3D12) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1486
R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1486
A:Status: translation not shown

A:Molecule type: mRNA
A:Residues: 1-140 <GIU>

A:Experimental source: hybridoma cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterodimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 34; DB 2; Length 140;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYFDS 10
DB 123 GSIFYFDN 129

RESULT 28

PH1499
ig heavy chain V region (clone X7-3D12H) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1499
R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have for somatic mutation

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1499
A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-140 <GIU>

A:Experimental source: hybridoma cell
C:Genetics:

A:introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterodimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 34; DB 2; Length 140;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYFDS 10
DB 123 GSIFYFDN 129

RESULT 29

E90868
hypothetical protein Ecs1917 [imported] - Escherichia coli (strain O157:H7, substrain R1)

C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: E90868

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
Gasaawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: E90868
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-204 <HAV>

A:Cross-references: UNIPROT:O8X8N7; GB:BA000007; PIDN:BA035340.1; PID:G13361382; GSPDB:G
C:Genetics:

A:Gene: Ecs1917

Query Match 63.0%; Score 34; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYY 7
DB 162 KLGTYY 167

RESULT 30

C70424
hypothetical protein aq_1428 - Aquifex aeolicus

C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: C70424

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: C70424
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-209 <AOQ>

A:Cross-references: UNIPROT:O67421; GB:AE000740; NID:G2983826; PIDN:AA07391.1; PID:G2983
C:Genetics:

A:Experimental source: strain VFS
A:Gene: aq_1428
C:Superfamily: Aquifex aeolicus hypothetical protein aq_1428

Query Match 63.0%; Score 34; DB 2; Length 209;
Best Local Similarity 63.6%; Pred. No. 65;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 2 KLGTYY 10
DB 121 KIGNTYTYFDT 131

RESULT 31

D85750
hypothetical protein z2431 [imported] - Escherichia coli (strain O157:H7, substrain EDL95)

C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85750

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lam, A.; Dolan, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: D85750
A:Status: preliminary

A:Molecule type: DNA

A;Residues: 1-230 <STO>
A;Cross-references: UNIPROT:Q8X8N7; GB:AE005174; NID:g12515422; PIDN:AAG56464.1; GSPDB:G
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z2431

Query Match 63.0%; Score 34; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTY 7
DB 188 KLGTY 193

RESULT 32
B81307
thiamin biosynthesis protein thig Cj1045c [similarity] - Campylobacter jejuni (strain NC
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81307
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barral
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: B81307
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <PAR>
A;Cross-references: UNIPROT:Q9PNE6; GB:AL139077; GB:AL111168; NID:96968444; PIDN:CA87330
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: thig; Cj1045c
C;Superfamily: thiamin biosynthesis protein thig

Query Match 63.0%; Score 34; DB 2; Length 258;
Best Local Similarity 60.0%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYPDS 10
DB 10 LKIGTYEFD 19

RESULT 33
A64659
outer membrane protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: A64659
R;Tom, J.F.; White, O.; Kervatage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalaf, H.G.; Giodok, A.; McKend
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: A64659
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-277 <TOM>
A;Cross-references: UNIPROT:Q25740; GB:AE000617; GB:AE000511; NID:92314256; PIDN:AAD0815
C;Genetics:
A;Start codon: TTG

Query Match 63.0%; Score 34; DB 2; Length 277;
Best Local Similarity 55.6%; Pred. No. 86;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYPD 9
DB 220 IKIPTYIFN 228

RESULT 34
B71856
probable outer membrane protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: B71856
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Miller, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: B71856
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <ARN>
A;Cross-references: UNIPROT:Q9ZKA1; GB:AE001532; GB:AE001439; NID:g4155628; PIDN:AAD0661;
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp1040

Query Match 63.0%; Score 34; DB 2; Length 277;
Best Local Similarity 55.6%; Pred. No. 86;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYPD 9
DB 220 IKIPTYIFN 228

RESULT 35
T08150
chitinase (EC 3.2.1.14) - Volvox carterii f. nagariensis
C;Species: Volvox carterii f. nagariensis
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T08150
R;Amou, P.; Haas, E.; Sumper, M.
Plant Cell 10, 781-789, 1998
A;Title: The sex-inducing pheromone and wounding trigger the same set of genes in the mu
A;Reference number: Z16381; MUID:98259000; PMID:9596636
A;Accession: T08150
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-309 <AMO>
A;Cross-references: UNIPROT:Q65213; EMBL:AF058716; NID:g3047412; PIDN:AAC13727.1; PID:g30
C;Keywords: glycosidase; hydrolase

Query Match 63.0%; Score 34; DB 2; Length 309;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYPD 9
DB 172 GTYYPD 177

RESULT 36
T48055
hypothetical protein F26K9.90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48055
R;Blaeker, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24465
A;Accession: T48055
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <BLO>
A;Cross-references: UNIPROT:Q9LZJ9; EMBL:AL162651
A;Experimental source: cultivar Columbia; BAC clone F26K9

C:Genetics:
A:Map position: 3
A:Note: F26K9.90

Query Match 63.0%; Score 34; DB 2; Length 357;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VKLGTYYFD 9
DB 132 LKLKYYFD 140

RESULT 37

membrane protein ydaH - Escherichia coli (strain K-12)

C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; PMID:97426617; PMID:9278503

A:Accession: C64883

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-510 <BLAT>

A:Cross-references: UNIPROT:P46133; GB:AE000231; GB:U00096; NID:g1787588; PIDN:AACT4418.

A:Experimental source: strain K-12, Substrains MG1655

C:Genetics:

A:Gene: ydaH

F:33-49/Domain: transmembrane #status predicted <TM01>

F:90-106/Domain: transmembrane #status predicted <TM02>

F:145-161/Domain: transmembrane #status predicted <TM03>

F:166-182/Domain: transmembrane #status predicted <TM04>

F:218-234/Domain: transmembrane #status predicted <TM05>

F:267-283/Domain: transmembrane #status predicted <TM06>

F:303-319/Domain: transmembrane #status predicted <TM07>

F:346-362/Domain: transmembrane #status predicted <TM08>

F:389-405/Domain: transmembrane #status predicted <TM09>

F:409-425/Domain: transmembrane #status predicted <TM10>

F:443-459/Domain: transmembrane #status predicted <TM11>

F:481-497/Domain: transmembrane #status predicted <TM12>

Query Match 63.0%; Score 34; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KLGTYY 7
DB 468 KLGTYY 473

RESULT 38

protein kinase (EC 2.7.1.37) - malaria parasite (Plasmodium falciparum)

N:Alternate names: calcium-dependent protein kinase

C:Species: Plasmodium falciparum

C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C:Accession: A45472; E71605; S28590

R:Zhao, Y.; Kappes, B.; Franklin, R.M.

J. Biol. Chem. 268, 4347-4354, 1993

A:Title: Gene structure and expression of an unusual protein kinase from Plasmodium falciparum

A:Reference number: A45472; PMID:93179444; PMID:8440720

A:Contents: KI

A:Accession: A45472

A:Molecule type: DNA

A:Residues: 1-524 <RHA>

A:Cross-references: UNIPROT:Q27731; EMBL:X67288; NID:g9877; PIDN:CAA47704.1; PID:g9878

A:Note: sequence extracted from NCBI backbone (NCBI:125849, NCBI:125850)

R:Gardner, M.J.; Tellez, H.; Carucci, D.D.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pitera, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.

Science 282, 1126-1132, 1998

A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A:Reference number: A71600; PMID:99021743; PMID:9804551

A:Accession: E71605

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-524 <GAR>

A:Cross-references: GB:AE001419; GB:AE001362; NID:g3845281; PIDN:AACT1952.1; PID:g3845284

A:Experimental source: clone 3D7

C:Genetics:

A:Gene: cpk; PFB0815w

A:Functions: 406/3; 440/1; 479/3; 505/3

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase C/keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific

F:54-325/Domain: protein kinase homology <KIN>

F:62-70/Region: protein kinase ATP-binding motif

F:46-48/Domain: calmodulin repeat homology <EF4>

Query Match 63.0%; Score 34; DB 2; Length 524;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VKLGTYYFD 9
DB 279 VEXKYYFD 287

RESULT 39

ABC-type transport protein cydD - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004

C:Accession: F64186

R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kiehlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Meidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; PMID:95350630; PMID:7542800

A:Accession: F64186

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-586 <TIGR>

A:Cross-references: UNIPROT:P45082; GB:U32795; GB:L42023; NID:g1574708; PIDN:AACT2812.1;

C:Genetics:

A:Gene: cydD

C:Superfamily: ATP-binding cassette homology

C:Keywords: ATP; nucleotide binding; P-loop; transmembrane protein; transport protein

F:23-39/Domain: transmembrane #status predicted <TM1>

F:66-82/Domain: transmembrane #status predicted <TM2>

F:145-161/Domain: transmembrane #status predicted <TM3>

F:167-183/Domain: transmembrane #status predicted <TM4>

F:252-268/Domain: transmembrane #status predicted <TM5>

F:285-301/Domain: transmembrane #status predicted <TM6>

F:366-557/Domain: ATP-binding cassette homology <ABC>

F:383-390/Region: nucleotide-binding motif A (P-loop)

Query Match 63.0%; Score 34; DB 2; Length 586;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 LGTYTYPD 9
DB 307 LGTYTYPD 313

RESULT 40

AD1818

N-acylglutaramoyl-L-alanine amidase [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:29:23 ; Search time 29.8876 Seconds
(without alignments)
192.513 Million cell updates/sec

Title: US-10-089-500-5
Perfect score: 54
Sequence: 1 VKLGYTFPS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot;
2: uniprot_trembl;

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	81.5	217	2 Q6LNK3	Q6LNK3 photobacter
2	44	81.5	217	2 CAG21123	CAG21123 photobact
3	43	79.6	456	2 Q97H36	Q97H36 clostridium
4	41	75.9	206	2 Q6LUP1	Q6LUP1 photobacter
5	41	75.9	206	2 CAG19074	CAG19074 photobact
6	41	75.9	704	2 Q8DKC6	Q8DKC6 synchococc
7	40	74.1	368	2 Q932E5	Q932E5 staphylococ
8	40	74.1	4130	2 Q7PIA2	Q7PIA2 chromobacte
9	39	72.2	434	2 Q6L4U1	Q6L4U1 oryza sativ
10	39	72.2	434	2 AAT38075	AAT38075 oryza sat
11	39	72.2	520	2 Q6QC13	Q6QC13 mint vein b
12	39	72.2	520	2 AAS57939	AAS57939 mint vein
13	39	72.2	565	2 Q74IS2	Q74IS2 lactobacill
14	39	72.2	565	2 AAS09261	AAS09261 lactobacil
15	39	72.2	2817	2 Q97K42	Q97K42 clostridium
16	38	70.4	262	2 Q8CPS5	Q8CPS5 staphylococ
17	38	70.4	281	2 Q8LTG9	Q8LTG9 staphylococ
18	38	70.4	405	2 Q8RAL5	Q8RAL5 thermotanas
19	38	70.4	587	1 COAT_PAVL3	P6310 parvovirus
20	38	70.4	587	2 Q84364	Q84364 murine minu
21	38	70.4	587	2 Q84367	Q84367 murine minu
22	38	70.4	716	1 COAT_MUMIV	P03117 murine minu
23	38	70.4	718	1 COAT_MUMIM	P07302 murine minu
24	38	70.4	729	2 Q84207	Q84207 murine minu
25	38	70.4	729	2 Q84366	Q84366 murine minu
26	38	70.4	847	2 Q55476	Q55476 synchococyt
27	38	70.4	907	2 Q9FW49	Q9FW49 arabidopsis
28	38	70.4	921	1 Y1B7_YEAST	P40547 saccharomyc
29	37	68.5	121	2 BAD00308	BAD00308 candida d
30	37	68.5	338	2 Q6CLB5	Q6CLB5 kluyveromyc
31	37	68.5	368	2 Q8QUM8	Q8QUM8 infectious

32	37	68.5	380	2 Q8WV03	Q8WV03 homo sapien
33	37	68.5	393	2 Q8NDI6	Q8NDI6 homo sapien
34	37	68.5	522	2 Q815Q4	Q815Q4 bacillus ce
35	37	68.5	529	2 Q8RCC8	Q8RCC8 thermotanas
36	37	68.5	798	2 Q9RKF0	Q9RKF0 streptomyces
37	37	68.5	814	2 Q80692	Q80692 arabidopsis
38	37	68.5	1101	2 Q8AB16	Q8AB16 bacteroides
39	36	66.7	149	2 Q6NSD8	Q6NSD8 rhodospheudo
40	36	66.7	149	2 CAE28482	CAE28482 rhodosphe
41	36	66.7	160	2 Q8DX46	Q8DX46 streptococc
42	36	66.7	203	1 YIAE_BACSU	YIAE_BACSU bacillus su
43	36	66.7	258	1 PLA3_PYRKO	PLA3_PYRKO pyrococcus
44	36	66.7	361	2 Q9V5K2	Q9V5K2 dirosophila
45	36	66.7	361	2 Q9L2Q3	Q9L2Q3 arabidopsis

ALIGNMENTS

RESULT 1
Q6LNK3 PRELIMINARY; PRT; 217 AA.
AC Q6LNK3;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedAccessionNames=BPAPA2751;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OX Vibrionaceae; Photobacterium.
RN NCBI_TaxID=74109;
RP SEQUENCE FROM N.A.
RA Verzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, CR378672; CAG21123.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 217 AA; 24557 MW; F477AC1AFA24BA6 CRC64;
QY 1 VKLGYTFPS 10
Db 155 VKLGYTFPS 164
Query Match 81.5%; Score 44; DB 2; Length 217;
Best Local Similarity 70.0%; Pred. No. 5.6;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
RESULT 2
ID CAG21123 PRELIMINARY; PRT; 217 AA.
AC CAG21123;
DT 10-MAY-2004 (T-EMBLrel. 27, Created)
DT 10-MAY-2004 (T-EMBLrel. 27, Last sequence update)
DT 10-MAY-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN PBPRA2751.
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OX Vibrionaceae; Photobacterium.
RN NCBI_TaxID=74109;
RP SEQUENCE FROM N.A.
RA Verzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome Analysis of Photobacterium profundum reveals the complexity of

RT	high pressure adaptations."
RL	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ss9;
RA	Cestaro A.;
RL	Submitted (MAR-2004) to the EMBL/Genbank/DDBJ databases.
DR	EMBL; CR378672; CAG31123.1; -.
KM	Hypothetical protein.
SQ	SEQUENCE 217 AA; 24557 MW; P477AC11AFA24BA6 CRC64;
QY	1 VKLGTYFFDS 10
DB	155 VKIGTHFDN 164
RESULT 3	
ID	097H36 PRELIMINARY; PRT; 456 AA.
AC	097H36;
DT	01-OCT-2001 (TREMBlrel. 18, Created)
DT	01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	Uncharacterized protein, CGEB homolog.
GN	OrderedlocusNames=CAC2177;
OS	Clostridium acetobutylicum
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC	Clostridium.
OX	NCBI_TaxID=1488;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX	MEDLINE=21359325; PubMed=11465286;
RX	DOI=10.1128/JB.183.16.4823-4838.2001;
RA	Noelling U., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA	Gibson R.J., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
RA	Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
RA	Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT	"Genome sequence and comparative analysis of the solvent-producing
RT	bacterium Clostridium acetobutylicum.";
RU	J. Bacteriol. 183:4823-4838(2001).
DR	EMBL; AE007718; AAK80135.1; -.
DR	PIR; D97168; D97168.
KW	Complete proteome.
SQ	SEQUENCE 456 AA; 53855 MW; 11BD94E1FB657F4 CRC64;
QY	1 VKLGTYFFDS 10
DB	380 IKENTYFDS 389
RESULT 4	
ID	06LUF1 PRELIMINARY; PRT; 206 AA.
AC	06LUF1;
DT	05-JUN-2004 (TREMBlrel. 27, Created)
DT	05-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT	05-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE	Hypothetical protein.
GN	OrderedlocusNames=PAPRA0653;
OS	Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC	Vibrionaceae; Photobacterium.
OX	NCBI_TaxID=74109;
RN	[1]

RA	SEQUENCE FROM N.A.
RP	Verzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA	Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA	Valle G.,
RT	"Genome analysis of Photobacterium profundum reveals the complexity of
RT	high pressure adaptations.";
RL	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; CR378665; CAG19074.1; -.
KW	Complete proteome; Hypothetical protein.
SO	SEQUENCE 206 AA; 23833 MW; 0F43398D786D3E77 CRC64;
QY	Query Match
	Best local Similarity 75.9%; Score 41; DB 2; Length 206;
	Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db	153 KIGTYPFET 161
RESULT 5	
ID	CAG19074 PRELIMINARY; PRT; 206 AA.
AC	CAG19074;
DT	10-MAY-2004 (TrEMBLrel. 27, Created)
DT	10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT	10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
GN	PBPRA0653.
OS	Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
CC	Vibrionaceae; Photobacterium.
OX	NCBI_TaxID=74109;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ss9;
RA	Verzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA	Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA	Valle G.,
RT	"Genome Analysis of Photobacterium profundum reveals the complexity of
RT	high pressure adaptations.";
RL	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ss9;
RA	Cestaro A.;
RL	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; CR378665; CAG19074.1; -.
KW	Hypothetical protein.
SO	SEQUENCE 206 AA; 23833 MW; 0F43398D786D3E77 CRC64;
QY	Query Match
	Best local Similarity 75.9%; Score 41; DB 2; Length 206;
	Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db	153 KIGTYPFET 161
RESULT 6	
ID	Q8DKC6 PRELIMINARY; PRT; 704 AA.
AC	Q8DKC6;
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	T110933 protein.
GN	OrderedlocusNames=T110933;
OS	Synechococcus elongatus (Thermosynechococcus elongatus).
OC	Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX	NCBI_TaxID=32046;
RN	[1]

RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneo T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Matenabe A., Iriuguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR EMBL, AP005372; BAC08485.1; -.
DR InterPro, IPR008258; SLT.
DR InterPro, IPR001440; TPR.
DR InterPro, IPR008941; TPR-1like.
DR Pfam, PF01464; SLT; 1.
DR PROSITE, PS50293; TPR_REGION; 1.
KM Complete proteome.
SQ SEQUENCE 704 AA; 81126 MW; 0DE8D9216268B52C CRC64;

Query Match 75.9%; Score 41; DB 2; Length 704;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLGYTFD 9
Db 627 IRLGTWYFD 635

RESULT 7
0932E5 PRELIMINARY; PRT; 368 AA.
ID 0932E5;
AC 0932E5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Int gene product.
GN Ordered locus names=SAV0783;
OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=2111952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshino K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi K., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
RT *aureus*.";
RL Lancet 357:1225-1240(2001).
DR EMBL, AP003360; BAB56945.1; -.
DR GO, GO:0003677; F:DNA binding; IEA.
DR GO, GO:0015074; P:DNA integration; IEA.
DR GO, GO:0006310; P:DNA recombination; IEA.
DR InterPro, IPR002110; ANK.
DR InterPro, IPR011010; DNA_bk_join_enz.
DR InterPro, IPR010998; L_intgrase_like_N.
DR InterPro, IPR002104; Phage integrase.
DR Pfam, PF00589; Phage integrase; 1.
DR PRINTS, PR01415; ANKTRIN.
KM Complete proteome.
SQ SEQUENCE 368 AA; 43818 MW; 14B83C72100292DE CRC64;

Query Match 74.1%; Score 40; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KLGTYYF 8
|||||

Db 16 KLGTYYF 22

RESULT 8
07PIA2 PRELIMINARY; PRT; 4130 AA.
ID 07PIA2;
AC 07PIA2;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Probable RTX (Repeat in structural toxin).
GN Ordered locus names=CV0311;
OS *Chromobacterium violaceum*.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882680; PubMed=14500782;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Crezynski-Paes T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinaceli F., Farib I.P., Felipe M.S.S., Ferrari L.P., Ferro U.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furian L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Geringeiro T.B.,
RA Grattapaglia D., Grizard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leal L.C.T., Lima L.F.A., Loureiro M.P., Lyra M.C.C.P.,
RA Madeira H.M.P., Manfro G.P., Maranhao A.O., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.V., Rondinelli B.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Suarez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Maesem R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of *Chromobacterium violaceum* reveals
RT remarkable and exploitable bacterial adaptability.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR EMBL, AE016911; AA057990.1; -.
DR GO, GO:0005009; F:calcium ion binding; IEA.
DR InterPro, IPR001343; Hemlyan_Ca_bind.
DR InterPro, IPR010221; VCSB.
DR Pfam, PF00353; Hemolyticbind; 4.
DR PRINTS, PR00313; CABDNCRPT.
DR TIGRFAMs, TIGR01965; VCSB_repeat; 25.
DR PROSITE, PS00330; HEMOLYSIN_CALCITM; 1.
KM Complete proteome.
SQ SEQUENCE 4130 AA; 431836 MW; E78381A3C0C6F00E CRC64;

Query Match 74.1%; Score 40; DB 2; Length 4130;
Best Local Similarity 70.0%; Pred. No. 5,5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VKLGYTFDS 10
Db 2460 VKXGTTFDS 2469

RESULT 9
06L4U1 PRELIMINARY; PRT; 434 AA.
ID 06L4U1;
AC 06L4U1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DR Hypothetical protein P0478F09.2.
GN Name=P0478F09.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Hsien Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-D., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; A0130610; AAT38075.1; -.
DR InterPro; IPR005037; PRP38.
DR Pfam; PF03371; PRP38; 1.
KW Hypothetical protein.
SQ SEQUENCE 434 AA; 51015 MW; A02AE70738E80CBF CRC64;

Query Match 72.2%; Score 39; DB 2; Length 434;
Best Local Similarity 87.5%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 LGTYFDS 10
DB 145 LGQYFDS 152

RESULT 10
AAT38075 PRELIMINARY; PRT; 434 AA.
AC AAT38075;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, last annotation update)
DE Hypothetical protein P0478F09.2.
GN P0478F09.2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza; Oryza sativa.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-D., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL "Oryza sativa PAC P0478F09 genomic sequence."
RT Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; A0130610; AAT38075.1; -.
KW Hypothetical protein.
SQ SEQUENCE 434 AA; 51015 MW; A02AE70738E80CBF CRC64;

Query Match 72.2%; Score 39; DB 2; Length 434;
Best Local Similarity 87.5%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 LGTYFDS 10
DB 145 LGQYFDS 152

RESULT 11
Q6QC13

ID Q6QC13 PRELIMINARY; PRT; 520 AA.
AC Q6QC13;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Polymerase (Fragment).
OS Mint vein banding virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC unassigned species in the family Closteroviridae.
OX NCBI_TaxID=265877;
RN [1]
RP SEQUENCE FROM N.A.
RA Tzanetakis I.E., Postman J.D., Martin R.R.;
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY548173; AAS57939.1; -.
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF00978; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 520 AA; 59370 MW; C0244E817FD86627 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 520;
Best Local Similarity 80.0%; Pred. No. 11e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 VKLGTYFDS 10
DB 426 VKLGKSYFDS 435

RESULT 12
AAS57939 PRELIMINARY; PRT; 520 AA.
AC AAS57939;
DT 25-MAR-2004 (TrEMBLrel. 27, Created)
DT 25-MAR-2004 (TrEMBLrel. 27, last sequence update)
DT 25-MAR-2004 (TrEMBLrel. 27, last annotation update)
DE Polymerase (Fragment).
OS Mint vein banding virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC unassigned species in the family Closteroviridae.
OX NCBI_TaxID=265877;
RN [1]
RP SEQUENCE FROM N.A.
RA Tzanetakis I.E., Postman J.D., Martin R.R.;
RL "Mint vein banding virus, a unique closterovirus infecting mint."
RT Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY548173; AAS57939.1; -.
FT NON TER 1
SQ SEQUENCE 520 AA; 59370 MW; C0244E817FD86627 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 520;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 VKLGTYFDS 10
DB 426 VKLGKSYFDS 435

RESULT 13
Q74IS2 PRELIMINARY; PRT; 565 AA.
AC Q74IS2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Prolyl-L-lysine synthetase.
GN OrderedListNames=LJ1493;
OS Lactobacillus johnsonii.

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxId=33959;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCC 533;
 RX PubMed=14966310;
 RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
 RA Pilet A.-C., Zwanen M.-C., Rouvet M., Altermann E., Barrangou R.,
 RA Mollet B., Mercenier A., Kleenhammer T., Arigoni F., Schell M.A.;
 RT "The genome sequence of the probiotic intestinal bacterium
 Lactobacillus johnsonii NCC 533.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
 CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
 DR EMBL: AE017204; AAS09261.1; -
 DR GO:0004812; F:RNA ligase activity; IEA.
 DR InterPro: IPR004154; HGTP_anticondon.
 DR InterPro: IPR004500; ProS_fam_11.
 DR InterPro: IPR002314; tRNA-synt_2b.
 DR InterPro: IPR006195; tRNA-synt_pro.
 DR InterPro: IPR007214; Ybak_1.
 DR Pfam: PF03129; HGTP_anticondon; 1.
 DR Pfam: PF0587; tRNA-synt_2b; 1.
 DR Pfam: PF04073; Ybak; 1.
 DR PRINTS: PR01046; TRNASYNTHPRO.
 DR TIGRFAMs: TIGR00409; pros_fam_11; 1.
 DR PROSITE: PS50862; AA_TRNA_LIGASE_11; 1.
 KW Aminoacyl-tRNA synthetase; Complete proteome.
 SQ SEQUENCE 565 AA; 63241 MW; F655C682A39D6BD4 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 565;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 KLGTYYFDS 10
 |||||
 Db 413 KLGTYYTDT 421

RESULT 14
 AAS09261 PRELIMINARY; PRT; 565 AA.
 ID AAS09261;
 AC AAS09261;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Prolyl-tRNA synthetase.
 GN Lj1493.
 OS Lactobacillus johnsonii.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxId=33959;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCC 533;
 RX PubMed=14966310;
 RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
 RA Pilet A.-C., Zwanen M.-C., Rouvet M., Altermann E., Barrangou R.,
 RA Mollet B., Mercenier A., Kleenhammer T., Arigoni F., Schell M.A.;
 RT "The genome sequence of the probiotic intestinal bacterium
 Lactobacillus johnsonii NCC 533.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
 DR EMBL: AE017204; AAS09261.1; -
 KW Aminoacyl-tRNA synthetase.
 SQ SEQUENCE 565 AA; 63241 MW; F655C682A39D6BD4 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 565;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 2 KLGTYYFDS 10
 |||||
 Db 413 KLGTYYTDT 421

Db 413 KLGTYYTDT 421

RESULT 15
 O97K42 PRELIMINARY; PRT; 2817 AA.
 ID O97K42;
 AC O97K42;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Uncharacterized protein, related to enterotoxins of other
 DE Clostridiales.
 GN OrderedLocNames=CAC1079;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxId=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=1466286;
 RX DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling U., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.T.,
 RA Tatubov R.L., Sabathe F., Doucet-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007623; AAK79053.1; -
 DR PIR: B97033; B97033.
 DR HSP: P06653; IHGX.
 DR InterPro: IPR002479; CW_binding.
 DR InterPro: IPR006626; Pbf1.
 DR Pfam: PF01473; CW_binding_1; 54.
 DR SMART: SM00710; Pbf1; 10.
 KW Complete proteome.
 SQ SEQUENCE 2817 AA; 318226 MW; 1851D0D4FFBEE921 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 2817;
 Best Local Similarity 70.0%; Pred. No. 5.8e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VKLGTYYFDS 10
 :|||
 Db 612 IKGNTYYFDS 621

RESULT 16
 O8CPFS PRELIMINARY; PRT; 262 AA.
 ID O8CPFS;
 AC O8CPFS;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Competence-damage inducible protein cna.
 GN OrderedLocNames=SB0962;
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RX PubMed=12950922;
 RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
 RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y.-M.,
 RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
 RT "Genome-based analysis of virulence genes in a non-biofilm-forming
 RT Staphylococcus epidermidis strain (ATCC 12228).";
 RL Mol. Microbiol. 49:1577-1593(2003).
 DR EMBL: AE016747; AAO04559.1; -
 DR GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
 DR InterPro: IPR001453; MocP_biosynth.

DR InterPro; IPR010920; Sm_like_riboprot.
KW COMPLETE proteome.
SQ SEQUENCE 262 AA; 29694 MW; C4B5FF6572CE347 CRC64;
Query Match 70.4%; Score 38; DB 2; Length 262;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 KLGTYYFDS 10
DB 124 RIGTYYFGS 132
RESULT 17
Q8LTC9 PRELIMINARY; PRT; 281 AA.
ID O8LTC9;
AC O8LTC9;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DE Hypothetical protein (Fragment).
OS Staphylococcus phage 187.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxId=55511;
RN [1]
RP SEQUENCE FROM N.A.
RA Panticek R., Oracova E., Kvardova V., Doskar J.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515457; AAM54032.1; -.
KW Hypothetical protein
FT NON_TER 281
SQ SEQUENCE 281 AA; 31326 MW; E6D0D2C8C0FA2790 CRC64;
Query Match 70.4%; Score 38; DB 2; Length 281;
Best Local Similarity 77.8%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLGTYYFDS 10
DB 244 KSGIYYFDS 252
RESULT 18
Q8RAL5 PRELIMINARY; PRT; 405 AA.
ID O8RAL5;
AC O8RAL5;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE ABC-type transport systems, involved in lipoprotein release, permease components.
GN OrderedLocustNames=TTB1198;
OS Orderediobacter tengcongensis.
OC Bacteriia; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxId=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; ARO13082; AAM24428.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003838; DUF214.
DR Pfam; PF02687; FtsX; 1.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 405 AA; 44689 MW; 0AC9708B2F873306 CRC64;
Query Match 70.4%; Score 38; DB 2; Length 405;

Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VKLGTYYF 8
DB 173 IKIGTYY 180
RESULT 19
COAT_PAVL3 STANDARD; PRT; 587 AA.
ID COAT_PAVL3
AC P363T0;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coat protein VP1 (Contains: Coat protein VP2).
OS Parvovirus luili.
OC Viruses; dsDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxId=35359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93297126; PubMed=8517025;
RA Difford N., Chen K.C., Bates R.C., Lederma M.;
RT "The complete nucleotide sequence of parvovirus luili and localization of a unique sequence possibly responsible for its encapsidation pattern."
RL Virology 192:339-345(1993).
CC -1- SIMILARITY: Belongs to the parvoviruses coat protein family.
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CC -----
DR EMBL; M81888; -; NOT_ANNOTATED_CDS.
DR PIR; B44276; B44276.
DR HSSP; P07302; 1MW.
DR InterPro; IPR001403; Parvo coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00740; Parvo_coat; 1.
KW Coat protein; Glycoprotein.
FT CARBOHYD 49 49
FT CARBOHYD 90 90
FT CARBOHYD 220 220
FT CARBOHYD 304 304
FT CARBOHYD 371 371
FT CARBOHYD 503 503
FT CARBOHYD 511 511
FT CARBOHYD 514 514
FT CARBOHYD 539 539
FT CARBOHYD 571 571
SQ SEQUENCE 587 AA; 52356B9CB2EBB74 CRC64;
Query Match 70.4%; Score 38; DB 1; Length 587;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTYYFDS 10
DB 267 GTYYFDT 273
RESULT 20
Q84364 PRELIMINARY; PRT; 587 AA.
ID Q84364;
AC Q84364;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE VP2 protein.


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GN Name=VP2;
OS Murine minute virus (Murine parvovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86115415; PubMed=3502703;
RA Astell C.R., Gardner E.M., Tattersall P.;
RT "DNA sequence of the lymphotropic variant of minute virus of mice,
RT MMV(1), and comparison with the DNA sequence of the fibrotropic
RT prototype strain.";
RL J. Virol. 57:656-669(1986).
DR EMBL; M12032; AAA69572.1; -.
DR HSSP; P30129; 4DPV.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat.1.
SQ SEQUENCE 587 AA; 64625 MW; 439FD2D9BC7C9782 CRC64;

Query Match
Beet Local Similarity 70.4%; Score 38; DB 2; Length 587;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTFPDS 10
DB 268 GTTFPDT 274

RESULT 21
084367 PRELIMINARY; PRT; 587 AA.
AC 084367;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE VPI protein.
GN Name=VPI;
OS Murine minute virus (Murine parvovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83143341; PubMed=6298737;
RA Astell C.R., Thomson M., Merchinsky M., Ward D.C.;
RT "The complete DNA sequence of minute virus of mice, an autonomous
RT parvovirus.";
RL Nucleic Acids Res. 11:999-1018(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=MVM;
RC MEDLINE=86115415; PubMed=3502703;
RA Astell C.R., Gardner E.M., Tattersall P.;
RT "DNA sequence of the lymphotropic variant of minute virus of mice,
RT MMV(1), and comparison with the DNA sequence of the fibrotropic
RT prototype strain.";
RL J. Virol. 57:656-669(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=MVM;
RC MEDLINE=87061199; PubMed=3783817;
RA Morgan W.R., Ward D.C.;
RT "Three splicing patterns are used to excise the small intron common to
RT all minute virus of mice RNAs.";
RL J. Virol. 60:1170-1174(1986).
DR EMBL; J02275; AAA67114.1; -.
DR HSSP; P30129; 4DPV.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR InterPro; IPR008975; Viral_cap_coat.

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DR Pfam; PF00740; Parvo_coat.1.
SQ SEQUENCE 587 AA; 64534 MW; 9B8A75280D755056 CRC64;

Query Match
Beet Local Similarity 70.4%; Score 38; DB 2; Length 587;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTFPDS 10
DB 268 GTTFPDT 274

RESULT 22
COAT MUMIV STANDARD; PRT; 716 AA.
ID COAT MUMIV
AC P03137;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coat protein VPI (Contains: Coat protein VP2).
OS Murine minute virus (Murine parvovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83143341; PubMed=6298737;
RA Astell C.R., Thomson M., Merchinsky M., Ward D.C.;
RT "The complete DNA sequence of minute virus of mice, an autonomous
RT parvovirus.";
RL Nucleic Acids Res. 11:999-1018(1983).
CC -1 SIMILARITY: Belongs to the parvoviruses coat protein family.
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CC -----
DR EMBL; V01115; CAA24310.1; ALT_SEQ.
DR PIR; A03700; VCPV2M.
DR HSSP; P07302; IMVM.
DR InterPro; IPR001403; Parvo_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00740; Parvo_coat.1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 716
FT FT 131 716 Coat protein VP2.
FT CARBOHYD 179 716 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 218 716 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 500 716 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 633 716 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 669 716 N-linked (GlcNAc...) (Potential).
FT DOMAIN 156 716 Gly-rich.
SQ SEQUENCE 716 AA; 78707 MW; 6A7229A91161F4C6 CRC64;

Query Match
Beet Local Similarity 70.4%; Score 38; DB 1; Length 716;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTFPDS 10
DB 397 GTTFPDT 403

RESULT 23
COAT MUMIM STANDARD; PRT; 718 AA.
ID COAT MUMIM
AC P07302; Q9WMH2; Q9WMH3;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)

```

DE Coat protein VP1 [Contains: Coat protein VP2].
 OS Murine minute virus (strain MMV1) (Murine parvovirus).
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
 OX NCBI_TaxId=10795;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86115415; PubMed=3502703;
 RA Astell C.R., Gardiner E.M., Tattersall P.;
 RT "DNA sequence of the lymphotropic variant of minute virus of mice,
 RT MMV(1), and comparison with the DNA sequence of the fibrotropic
 RT prototype strain.";
 RL J. Virol. 57:656-669(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85242059; PubMed=3855242;
 RA Sahli R., McMaster G.K., Hirt B.;
 RT "DNA sequence comparison between two tissue-specific variants of the
 RT autonomous parvovirus, minute virus of mice.";
 RL Nucleic Acids Res. 13:3617-3633(1985).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 132-718.
 RA Llamas-Saiz A.L., Agbandje-Mckenna M., Wikoff W.R., Bratton J.,
 RA Tattersall P., Rossmann M.G.;
 RT "Structure determination of Minute Virus of mice.";
 RL Acta Crystallogr. D 53:93-100(1997).
 CC -1- SIMILARITY: Belongs to the parvoviruses coat protein family.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X02481; CAB46507.1; -;
 DR EMBL: X02481; CAB46508.1; -;
 DR EMBL: M12032; AAA69569.1; ALT_INIT.
 DR PIR: B23008; VCPVIM.
 DR PDB: 1MVM; X-ray; A=132-718.
 DR InterPro: IPR001403; Parvo coat.
 DR InterPro: IPR008975; Viral_cap_coat.
 DR Pfam: PF00740; Parvo_coat; 1.
 KW 3D-structure; Coat protein; Glycoprotein.
 KM 3D-structure; Coat protein; Glycoprotein.
 FT CHAIN 1 718
 FT CARBOHYD 132 718
 FT CARBOHYD 180 180
 FT CARBOHYD 219 219
 FT CARBOHYD 502 502
 FT CARBOHYD 635 635
 FT CARBOHYD 671 671
 FT DOMAIN 157 172
 FT CONFILCT 144 144
 FT STRAND 182 186
 FT STRAND 191 204
 FT STRAND 213 217
 FT TURN 220 221
 FT TURN 228 231
 FT STRAND 235 245
 FT TURN 251 253
 FT TURN 251 253
 FT HELIX 256 265
 FT STRAND 266 266
 FT STRAND 268 269
 FT STRAND 274 289
 FT STRAND 296 301
 FT TURN 303 304
 FT STRAND 307 307
 FT STRAND 309 312
 FT STRAND 322 325
 FT HELIX 326 326
 FT TURN 333 334
 FT TURN 337 338
 FT STRAND 340 345

FT STRAND 351 351
 FT TURN 357 358
 FT STRAND 367 367
 FT TURN 373 375
 FT HELIX 381 384
 FT STRAND 390 390
 FT STRAND 396 397
 FT STRAND 408 409
 FT STRAND 428 428
 FT STRAND 438 438
 FT HELIX 442 444
 FT TURN 458 460
 FT STRAND 466 467
 FT TURN 473 474
 FT STRAND 477 477
 FT STRAND 484 484
 FT TURN 494 494
 FT TURN 499 503
 FT STRAND 509 509
 FT TURN 512 513
 FT STRAND 525 525
 FT STRAND 534 536
 FT HELIX 546 546
 FT STRAND 557 558
 FT TURN 559 559
 FT STRAND 575 577
 FT TURN 583 584
 FT STRAND 585 586
 FT STRAND 600 600
 FT STRAND 618 618
 FT STRAND 627 630
 FT STRAND 636 636
 FT STRAND 649 649
 FT STRAND 652 668
 FT STRAND 683 683
 FT STRAND 691 691
 FT HELIX 692 694
 SQ SEQUENCE 718 AA; 79017 MW; B43C1762ED5F74B9 CRC64;
 Query Match 70.4%; Score 38; DB 1; Length 718;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GTYFDS 10
 Db 399 GTYFDT 405
 ID 084207 PRELIMINARY; PRT; 723 AA.
 AC 084207;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Coding sequence.
 OS Murine minute virus (Murine parvovirus).
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
 OX NCBI_TaxId=10794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83143341; PubMed=6298737;
 RA Astell C.R., Thomson M., Merchinsky M., Ward D.C.;
 RT "The complete DNA sequence of minute virus of mice, an autonomous
 RT parvovirus.";
 RL Nucleic Acids Res. 11:999-1018(1983).
 DR EMBL: V01115; CA24313.1; -;
 DR HSSP: P30129; 4DPV.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0005198; P:structural molecule activity; IEA.
 DR InterPro: IPR001403; Parvo coat.
 DR InterPro: IPR008975; Viral_cap_coat.
 DR Pfam: PF00740; Parvo_coat; 1.

SO SEQUENCE 723 AA; 79492 MW; F805707524126980 CRC64;
 Query Match 70.4%; Score 38; DB 2; Length 723;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 GTTYFDS 10
 |||||:
 404 GTTYFDT 410

RESULT 25
 OQ4366 PRELIMINARY; PRT; 729 AA.
 ID OQ4366;
 AC OQ4366;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE VPI protein.
 GN Name=VPI;
 OS Murine minute virus (Murine parvovirus).
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
 OX NCBI_TaxID=10794;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MV;
 RX MEDLINE=83143341; PubMed=6298737;
 RT "The complete DNA sequence of minute virus of mice, an autonomous parvovirus.";
 RL Nucleic Acids Res. 11:999-1018(1983).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MV;
 RX MEDLINE=86115415; PubMed=3502703;
 RA Astell C.R., Gardiner E.M., Tattersall P.;
 RT "DNA sequence of the lymphotropic variant of minute virus of mice, MVM(1), and comparison with the DNA sequence of the fibrocytic RT prototype strain.";
 RL J. Virol. 57:656-669(1986).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MV;
 RX MEDLINE=87061199; PubMed=3783817;
 RA Morgan W.R., Ward D.C.;
 RT "Three splicing patterns are used to excise the small intron common to all minute virus of mice RNAs.";
 RL J. Virol. 60:1170-1174(1986).
 DR EMBL; J02275; AAA67111.1; -.
 DR HSP; J30129; ADPV.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR001403; ViroL_Cap_coat.
 DR Pfam; PF00740; Parvo_coat.1.
 SQ SEQUENCE 729 AA; 80145 MW; CCE2686A03CB6AB CRC64;

Query Match 70.4%; Score 38; DB 2; Length 729;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 GTTYFDS 10
 |||||:
 410 GTTYFDT 416

RESULT 26
 OQ5476 PRELIMINARY; PRT; 847 AA.
 ID OQ5476;
 AC OQ5476;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Soluble lytic transglycosylase.
 GN Name=slc; OrderedLocustNames=slr0534;
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T., Hoshino T., Matsumoto A., Muraki A., Nakazaki N., Kato K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yabuta M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugita M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb DNA Res. 2:153-166(1995).
 DR EMBL; D64006; BAA10822.1; -.
 DR PIR; S75975; S75975.
 DR InterPro; IPR008258; SLT.
 DR InterPro; IPR008941; TPR-1like.
 DR Pfam; PF01464; SLT; 1.
 KW Complete proteome.
 SQ SEQUENCE 847 AA; 95980 MW; A84B878873BE00AF CRC64;

Query Match 70.4%; Score 38; DB 2; Length 847;
 Best Local Similarity 66.7%; Pred. No. 2.8e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VKLGTTFD 9
 |||||:
 759 VNMGTTFD 767

RESULT 27
 OQFW49 PRELIMINARY; PRT; 907 AA.
 ID OQFW49;
 AC OQFW49;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein T184.10.
 GN Name=T184.10;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uteback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBD databases.
 DR EMBL; AC069299; AAG26079.1; -.
 DR PIR; A86460; A86460.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR Pfam; PF00560; LRR; 21.
 DR PRINTS; PR00019; LEURICHRPT.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
 KW Hypothetical protein.

SQ SEQUENCE 907 AA; 99876 MW; 60BA983FB32F0009 CRC64;
 Query Match 70.4%; Score 38; DB 2; Length 907;
 Best Local Similarity 85.7%; Pred. No. 3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTRYFDS 10
 DB 795 GTRYFDS 801

RESULT 28
 Y1B7_YEAST STANDARD; PRT; 921 AA.
 ID Y1B7_YEAST
 AC P40547;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical 105.5 kDa protein in RPL2B-SNL1 intergenic region.
 GN OrderedLocustNames=Y11017C;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NC NCBI_TaxID=4932;
 RX MEDLINE=8288c / AB972;
 RA Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
 RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
 RA Harris D.E., Hornsell T., Hunt S., Jagsis K., Jones M., Lyne G.,
 RA Moulé S., O'Neill C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
 RA Skelton J., Smith V., Walsh S., Whitehead S., Barrett B.G.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
 RL Nature 387:84-87 (1997).
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 CC -----
 CC EMBL; 246881; CA86975.1; -.
 DR PIR; S49965; S49965.
 DR GERMOnline; 139554; -.
 DR SGD; S0001279; Y11017C.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0045721; P:negative regulation of gluconeogenesis; IMP.
 DR InterPro; IPR008938; ARM.
 KM Hypothetical protein.
 SQ SEQUENCE 921 AA; 105491 MW; DDFAS50E22E846A0 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 921;
 Best Local Similarity 85.7%; Pred. No. 3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYTFD 9
 DB 72 VGTTFD 78

RESULT 29
 BAD00308 PRELIMINARY; PRT; 121 AA.
 ID BAD00308;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE Immunoglobulin heavy chain VHDJ region (Fragment).
 GN IGVH.

OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 NC NCBI_TaxID=9838;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Honda T., Akahori Y., Kurosawa Y.;
 RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
 RT gamma3 in vivo repertoires."
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB091946; BAD00308.1; -.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 121 AA; 12879 MW; 10BCB007D5AE7FAD CRC64;

Query Match 68.5%; Score 37; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTRYFDS 9
 DB 53 GTRYFDS 58

RESULT 30
 06CLB5 PRELIMINARY; PRT; 338 AA.
 ID 06CLB5;
 DT 01-OCT-2004 (TEMBLrel. 28, Created)
 DT 01-OCT-2004 (TEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TEMBLrel. 28, Last annotation update)
 DE Similar to sp|P38235|Saccharomyces cerevisiae YBR053c singleton.
 GN ORFNames=K1LA0P043015;
 GN Kluveromyces lactic (Yeast).
 OS Kuyveromyces; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kuyveromyces.
 NC NCBI_TaxID=28985;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RC GENOEVOLRES;
 RA Dujon B., Sherman D., Fischer G., Durens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
 RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissrame A., Boyer J., Catolico L., Confanioleri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogiropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swenne D., Tekala F., Weslowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44 (2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382126; CAG97982.1; -.
 SQ SEQUENCE 338 AA; 38362 MW; DBD1603F135D96D5 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 338;
 Best Local Similarity 77.8%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYFDS 10
 DB 10 KNGPYFDS 18

RESULT 31
 O8QUM6 PRELIMINARY; PRT; 368 AA.
 AC O8QUM6; 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE ORF082L.
 OS Infectious spleen and kidney necrosis virus.
 OC unclassified Iridoviridae.
 NCBI_TaxID=180170;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21874810; PubMed=11878882;
 RA He J.G., Deng M., Weng S.P., Li Z., Zhou S.Y., Long Q.X., Wang X.Z.,
 Chan S.M.;
 RT "Complete genome analysis of the mandarin fish infectious spleen and
 kidney necrosis iridovirus."
 RL Virology 291:126-139(2001).
 DR EMBL: AF771960; AAL98806.1; -
 SQ SEQUENCE 368 AA; 40658 MW; D8E08B028DDA0CE6 CRC64;
 Query Match 68.5%; Score 37; DB 2; Length 368;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LGTYPFDS 10
 DB 231 KMGTYRYS 239
 RESULT 32
 O8WV03 PRELIMINARY; PRT; 380 AA.
 AC O8WV03; 01-MAR-2002 (TEMBLrel. 20, Created)
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
 DT 01-OCT-2004 (TEMBLrel. 28, Last annotation update)
 DE Hypothetical protein FLJ35155.
 GN Name=FLJ35155;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon, and Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 Diatchenko L., Marzula K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Useth T.B., Tothyluk S., Cerantoni P., Prange C.J.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
 Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fehey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
 Krzyzinski M.I., Skalka U., Smalls D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC019036; AAL19036.1; -
 DR EMBL: BC039067; AAL39067.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 380 AA; 42510 MW; 108A64F4EAF8F3F CRC64;
 Query Match 68.5%; Score 37; DB 2; Length 380;
 Best Local Similarity 87.5%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 LGTYPFDS 10
 DB 183 LGTYSDS 190
 RESULT 33
 O8NB16 PRELIMINARY; PRT; 393 AA.
 AC O8NB16; 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Hypothetical protein PSEC0251.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayaishi K., Ishii S.,
 Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
 RA Nagahara K., Sugano S., Isogai T.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK075551; BAC11694.1; -
 SQ SEQUENCE 393 AA; 43806 MW; 3C788AFD933A23D CRC64;
 Query Match 68.5%; Score 37; DB 2; Length 393;
 Best Local Similarity 87.5%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 LGTYPFDS 10
 DB 196 LGTYSDS 203
 RESULT 34
 O81S04 PRELIMINARY; PRT; 522 AA.
 AC O81S04; 01-JUN-2003 (TEMBLrel. 24, Created)
 DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE NADH oxidase (NOXASE) (EC 1.6.99.3).
 GN ORFNames=BC5081;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 NCBI_TaxID=226900;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Yanova N., Sorokin A., Anderson I., Gallerton N., Candelon B.,
 Reparat V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
 Chu L., Mazur M., Goldsman E., Larsen N., D'Souza M., Malinas T.,
 Greckin Y., Pusch G., Haselkorn R., Fontein M., Ehrlich S.D.,
 Overbeek R., Kyriides N.C.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with

```
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL: AE017014; AAP11950.1; -.
DR GO: GO:0003954; F:NADH dehydrogenase activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
KM Oxidoreductase.
SQ SEQUENCE 522 AA; 61087 MW; 551097794F59855 CRC64;

Query Match
Best Local Similarity 66.7%; Score 37; DB 2; Length 522;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGYTFD 9
DB 127 IKSGLYTFD 135

RESULT 35
08RC8 PRELIMINARY; PRT; 529 AA.
ID 08RC8;
AC 08RC8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Flagellar capping protein.
GN Name=Flid; OrderedLocNames=TFE0505;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OC NCBI_TaxID=119072;
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=21992816; Pubmed=11997336;
RA Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome."
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013021; AAM23784.1; -.
DR GO: GO:0009288; C:flagellum (sensu Bacteria); IEA.
DR GO: GO:0009296; P:flagellum biogenesis; IEA.
DR GO: GO:0009296; P:flagellum biogenesis; IEA.
DR InterPro: IPR010810; Flagellin_IN.
DR InterPro: IPR010809; Flid_C.
DR InterPro: IPR003481; Flid_N.
DR Pfam: PF07196; Flagellin_IN; 1.
DR Pfam: PF07195; Flid_C; 1.
DR Pfam: PF02465; Flid_N; 1.
KM Complete proteome; Flagellum.
SQ SEQUENCE 529 AA; 58032 MW; 1F31EB53C1623A19 CRC64;

Query Match
Best Local Similarity 66.7%; Score 37; DB 2; Length 529;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYTFD 10
DB 126 KIGAVYIDS 134

RESULT 36
09RKF0 PRELIMINARY; PRT; 798 AA.
ID 09RKF0;
AC 09RKF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-UN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative hydrolase.
GN OrderedLocNames=SC03487; ORFNames=SCB65_23;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinaceae; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=1902;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; Pubmed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kiese H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kiese T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wierozorek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)."
RL Nature 417:141-147(2002).
DR EMBL: AL939116; CAB61811.1; -.
DR GO: GO:0016787; F:hydrolase activity; IEA.
KM Complete proteome; Hydrolase.
SQ SEQUENCE 798 AA; 88594 MW; 47244CF6FC555C CRC64;

Query Match
Best Local Similarity 100.0%; Score 37; DB 2; Length 798;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYTFD 9
DB 157 GTYTFD 162

RESULT 37
080692 PRELIMINARY; PRT; 814 AA.
ID 080692;
AC 080692;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE F8K4.5 protein.
GN Name=F8K4.5;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Kwan A., Yu G., Oji O.,
RA Liu S., Li J., Arzajo R., Au M., Brendel V., Buehler E., Conway A.B.,
RA Conway A.R., Dewar K., Feng J., Kim C., Kuritz D., Li Y., Palm C.J.,
RA Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.;
RA Theologis A.;
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Theologis;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Theologis;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC004392; AAC28517.1; -.
DR PIR: T02130; T02130.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR011424; Cl_3.
DR InterPro: IPR002219; DAG_Pf-bind.
DR InterPro: IPR004146; DCl.
DR InterPro: IPR011011; FYVE_Phd_ZnF.
DR InterPro: IPR000834; Peptidase_M14.
DR InterPro: IPR001965; ZnF_Phd.
DR Pfam: PF03107; Cl_2; 3.
DR Pfam: PF07649; Cl_3; 4.
```

DR SMART; SM00109; C1; 2.
 DR SMART; SM00249; PHD; 4.
 DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN 1.
 SQ SEQUENCE 814 AA; 93000 MW; EE8E79A280002C74 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 814;
 Best Local Similarity 70.0%; Pred. No. 4.1e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VKLGYTFDS 10
 DB 758 LKLGKTYFDS 767

RESULT 38

OBAB16 PRELIMINARY; PRT; 1101 AA.
 AC OBAB16;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative xanthan lyase XalB.
 GN Ordered locus names=BT0296;
 OS Bacteroides thetaiotaomicron.
 OC Bacterioides; Bacteroidetes; Bacteroidales;
 OC Bacteroidaceae; Bacterioides.
 OX NCBI_Taxid=816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE=22550858; PubMed=12663928;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RL Science 299:2074-2076(2003).
 DR EMBL; AE016927; AA075403.1; -;
 DR GO; GO:0016829; F1-lyase activity; IEA.
 KW Complete proteome; Lyase.
 SQ SEQUENCE 1101 AA; 127580 MW; 6B3BE78F465E6E09 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 1101;
 Best Local Similarity 66.7%; Pred. No. 5.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KLGTYFDS 10
 DB 1067 QLGTYFSA 1075

RESULT 39
 O6N5D8 PRELIMINARY; PRT; 149 AA.
 AC O6N5D8;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN Ordered locus names=RPA3041;
 OS Rhodopseudomonas palustris.
 OC Bacterioides; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_Taxid=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Perez C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodopseudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004).
 KW Complete proteome; Rhodopseudomonas palustris.

DR EMBL; BX572602; CAE28482.1; -;
 DR InterPro; IPR007301; DoxD.
 DR InterPro; IPR011592; Surf4_rel.
 DR Pfam; PF04173; Doxd; 1.
 DR Prodom; PD010195; Surf4_rel; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 149 AA; 15385 MW; 3D765810D9228D43 CRC64;

Query Match 66.7%; Score 36; DB 2; Length 149;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VKLGYTF 8
 DB 98 VAIGTYF 105

RESULT 40

CAE28482 PRELIMINARY; PRT; 149 AA.
 ID CAE28482;
 AC CAE28482;
 DT 02-MAR-2004 (TREMBLrel. 27, Created)
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN RPA3041.
 OS Rhodopseudomonas palustris.
 OC Bacterioides; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_Taxid=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Perez C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodopseudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572602; CAE28482.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 149 AA; 15385 MW; 3D765810D9228D43 CRC64;

Query Match 66.7%; Score 36; DB 2; Length 149;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VKLGYTF 8
 DB 98 VAIGTYF 105

Search completed: December 17, 2004, 19:14:38
 Job time : 30.8876 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:10:02 ; Search time 33.4326 Seconds
(without alignments)
118.029 Million cell updates/sec

Title: US-10-089-500-6
Perfect score: 54
Sequence: 1 SASODISNYLN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	11	2	AAW70614
2	54	100.0	11	4	AAAB1982
3	54	100.0	11	5	ABPE1183
4	54	100.0	11	6	ABU11007
5	54	100.0	103	7	ADFO9995
6	54	100.0	103	7	ADFI10099
7	54	100.0	107	2	AAW68804
8	54	100.0	107	2	AAW68805
9	54	100.0	107	2	AAW70623
10	54	100.0	107	2	AAW70625
11	54	100.0	107	5	ABPE1192
12	54	100.0	107	5	ABPE1194
13	54	100.0	108	2	AAW70620
14	54	100.0	108	2	AAW70618
15	54	100.0	108	2	AAW70696
16	54	100.0	108	4	AAAB1988
17	54	100.0	108	4	AAAB1986
18	54	100.0	108	4	AAAB1990
19	54	100.0	108	5	ABPE1189
20	54	100.0	108	5	ABPE1265
21	54	100.0	108	5	ABPE1187
22	54	100.0	108	6	ABU11011
23	54	100.0	108	6	ABU11013
24	54	100.0	108	8	ADG31770
25	54	100.0	108	8	ADG31782

26	54	100.0	108	8	ADG31768	Adg31768 V(L) doma
27	54	100.0	108	8	ADG31893	Adg31893 V(L) proc
28	54	100.0	110	2	AAW70673	AAW70673 Anti-VEGF
29	54	100.0	110	2	AAW70677	AAW70677 Anti-VEGF
30	54	100.0	110	2	AAW70687	AAW70687 Anti-VEGF
31	54	100.0	110	2	AAW70675	AAW70675 Anti-VEGF
32	54	100.0	110	3	AAAB05897	AAAB05897 Humanised
33	54	100.0	110	3	AAAB13380	AAAB13380 Anti-VEGF
34	54	100.0	110	3	AAAB13376	AAAB13376 F(ab)-12
35	54	100.0	110	5	ABPE1242	ABPE1242 Humanised
36	54	100.0	110	5	ABPE1256	ABPE1256 Humanised
37	54	100.0	110	5	ABPE1244	ABPE1244 Humanised
38	54	100.0	110	5	ABPE1246	ABPE1246 Humanised
39	54	100.0	128	2	AAAB33257	AAAB33257 Rat Immun
40	54	100.0	128	2	AAAB33340	AAAB33340 KM641 H C
41	54	100.0	128	2	AAAB28368	AAAB28368 pCM641 LA
42	54	100.0	128	3	AAAB01628	AAAB01628 Murine im
43	54	100.0	128	4	AAAB1994	AAAB1994 Gangliost
44	54	100.0	128	4	AAAB1995	AAAB1995 Gangliost
45	54	100.0	128	4	AAAB1997	AAAB1997 Gangliost

ALIGNMENTS

RESULT 1	AAW70614	standard; peptide; 11 AA.
ID	AAW70614	
XX	AAW70614	
AC	AAW70614	
DT	27-JAN-1999	(first entry)
XX		
DE	Anti-VEGF antibody light chain hypervariable region CDR1.	
XX		
KW	light chain hypervariable region; murine; humanised antibody;	
KM	anti-vascular endothelial growth factor antibody; anti-VEGF antibody;	
KW	VEGF-induced angiogenesis; tumour; retinal disorder;	
KM	age-related macular degeneration; diabetic retinopathy;	
XX	rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.	
OS	Synthetic.	
OS	Mus sp.	
XX		
PN	MO9845331-A2.	
XX		
PD	15-OCT-1998.	
XX		
PF	03-APR-1998; 98WO-US006604.	
XX		
PR	07-APR-1997; 97US-00833504.	
PR	06-AUG-1997; 97US-00908469.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;	
XX		
DR	WPI; 1998-568337/48.	
XX		
PT	New humanised antibody with affinity for vascular endothelial growth	
PT	factor - for treatment of tumours, retinal disease and other angiogenic	
PT	states, also related nucleic acid, vectors and transformed cells.	
XX		
PS	Claim 9; Page 80; 100pp; English.	
XX		
CC	The present sequence represents a light chain hypervariable region of the	
CC	murine anti-vascular endothelial growth factor (anti-VEGF) antibody. The	
CC	sequence is used to construct the humanised anti-VEGF antibody of the	
CC	invention. The humanised antibodies are used to inhibit VEGF-induced	
CC	angiogenesis, particularly for treating or preventing tumours (of any	
CC	type) and retinal disorders (e.g. age-related macular degeneration or	
CC	diabetic retinopathy). They can also be used to treat other conditions	
CC	that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,	

CC atherosclerosis, Grave's disease, etc
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 54; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASQDISNYLN 11
DB 1 SASQDISNYLN 11
RESULT 2
AAB81982
ID AAB81982 standard; peptide; 11 AA.
XX
AC AAB81982;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related peptide SEQ ID NO: 6.
XX
KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
OS Mus musculus.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 4; Page 141; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 54; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASQDISNYLN 11
DB 1 SASQDISNYLN 11
RESULT 3
ABP61183
ID ABP61183 standard; peptide; 11 AA.
XX
AC ABP61183;
XX

DT 20-SEP-2002 (first entry)
XX
DE Humanised anti-VEGF antibody light chain hypervariable domain, CDRL1.
XX
KM Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KM vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KM retinal disorder; intracocular neovascular disorder; light chain;
KM hypervariable domain; CDRL1.
XX
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PN US2002032315-A1.
XX
PD 14-MAR-2002.
XX
PF 06-APR-1998; 98US-00056160.
XX
PR 06-AUG-1997; 97US-0054856P.
XX
XX (BACA/) BACA M.
PA (WELL/) WELLS J A.
PA (PREST/) PRESTA L G.
PA (LOKMAN/) LOKMAN H B.
PA (CHEN/) CHEN Y M.
XX
PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX
DR WPI; 2002-517920/55.
XX
XX
PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.
XX
XX
PS Claim 9; Page 31; 47pp; English.
XX
XX
CC The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
CC particularly those having a tumour or a retinal disorder e.g. intracocular
CC neovascular disorders. The present sequence is an exemplary light chain
CC hypervariable domain of the humanised anti-VEGF antibody of the invention
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 54; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASQDISNYLN 11
DB 1 SASQDISNYLN 11
RESULT 4
ABU11007
ID ABU11007 standard; peptide; 11 AA.
XX
AC ABU11007;
XX
DT 04-FEB-2003 (first entry)
XX
DE Modified ganglioside GD3 antibody associated peptide #4.
XX
XX
KM Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS Mus musculus.
XX
PN WO200278739-A1.
XX
PD 10-OCT-2002.

XX 29-MAR-2002; 2002WO-JP003170.
PF physico-chemical property of an antibody by a computational screening
XX method. The method comprises: receiving a template antibody structure;
PR 29-MAR-2001; 2001JP-00097483.
XX selecting at least one variable position belonging to the antibody
XX structure; selecting at least one amino acid to be considered at the
XX variable position(s); analyzing the interaction of each selected amino
PI Shitara K, Niwa R, Kanazawa J, Asada M;
DR MPI; 2003-067410/06.
XX antibody, including the selected amino acids at other variable positions;
XX and identifying a set of at least one antibody sequence with at least one
PT optimized physico-chemical property. The method is useful for optimizing
XX the physico-chemical properties of an antibody, especially the stability,
XX solubility, or antigen binding affinity. The optimized antibody may be
XX useful for treating a patient. The present sequence is an antibody
XX variable region sequence used to illustrate the invention.
PS Claim 6; Page 99; 121pp; Japanese.
SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASODISNYLN 11
DB 1 SASODISNYLN 11

RESULT 5

ADFO9995
ID ADFO9995 standard; protein; 103 AA.

XX ADFO9995;

DT 12-FEB-2004 (first entry)

XX Antibody light chain variable region 1CZ8(1D-33).

XX Antibody; stability; solubility; antigen binding affinity;

KW variable region; human.

XX Homo sapiens.

OS WO2003074679-A2.

PN 12-SEP-2003.

PD 03-MAR-2003; 2003WO-US006598.

XX 01-MAR-2002; 2002US-0360843P.

PR 29-MAY-2002; 2002US-0384197P.

XX (XENC-) XENCOR.

PA Lazar GA, Desjarlais JR, Marshall SA, Dahiya B;

PI MPI; 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
XX positions.
XX Disclosure; Fig 2b; 135pp; English.

CC The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.
SQ Sequence 103 AA;

Query Match 100.0%; Score 54; DB 7; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34

RESULT 6

ADFI0099
ID ADFI0099 standard; protein; 103 AA.

XX ADFI0099;

DT 12-FEB-2004 (first entry)

XX VEGF antibody light chain variable region 1CZ8.

XX Antibody; stability; solubility; antigen binding affinity;

KW variable region; human; VEGF.

XX Homo sapiens.

OS WO2003074679-A2.

PN 12-SEP-2003.

PD 03-MAR-2003; 2003WO-US006598.

XX 01-MAR-2002; 2002US-0360843P.

PR 29-MAY-2002; 2002US-0384197P.

XX (XENC-) XENCOR.

PA Lazar GA, Desjarlais JR, Marshall SA, Dahiya B;

PI MPI; 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
XX positions.
XX Example 6; Fig 16b; 135pp; English.

CC The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,

CC solubility, or antigen binding affinity. The optimized antibody may be
 CC useful for treating a patient. The present sequence is an antibody
 CC variable region sequence used to illustrate the invention.
 XX
 SQ Sequence 103 AA;

Query Match 100.0%; Score 54; DB 7; Length 103;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASODISNYLN 11
 |||||
 DB 24 SASODISNYLN 34

RESULT 7
 AAW6804
 ID AAW6804 standard; protein; 107 AA.

AC AAW6804;

DT 26-FEB-1999 (first entry)

DE Variable light domain 1.

XX Complementarily-determining regions; CDRs; murine; antibody; VEGF;
 KW vascular endothelial growth factor; humanised antibody; tumour;
 KM mitogenic.

XX Homo sapiens.

XX WO9845332-A2.

XX 15-OCT-1998.

PF 03-APR-1998; 98WO-US006724.

PR 07-APR-1997; 97US-00833504.

PA (GETH) GENENTECH INC.

PI Wells JA, Baca M, Presta LG;

DR WPI; 1998-594479/50.

XX New humanised antibody with specific alterations in human framework -
 PT specifically reactive with vascular endothelial growth factor, useful for
 PT inhibiting tumour growth.

PS Claim 6; Page 30-31; 45pp; English.

XX AAW6804 is the variable light region of the humanised A4.6.1 variant
 CC hu2.0. This variant contains only the complementarily-determining regions
 CC (CDRs) from the murine antibody grafted on to a human light chain K
 CC subgroup I and heavy chain subgroup III framework. Antibodies are
 CC especially reactive with vascular endothelial growth factor (VEGF) and
 CC are used to inhibit growth of tumours by inhibiting mitogenic signalling
 CC

SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASODISNYLN 11
 |||||
 DB 24 SASODISNYLN 34

RESULT 8
 AAW6805
 ID AAW6805 standard; protein; 107 AA.

AC AAW6805;
 XX
 DT 26-FEB-1999 (first entry)
 XX
 DE Variable light domain 2.

XX Antibody; VEGF; vascular endothelial growth factor; humanised antibody;
 KW tumour; mitogenic; phage sorting.
 XX

OS Homo sapiens.

XX WO9845332-A2.

XX 15-OCT-1998.

PF 03-APR-1998; 98WO-US006724.

PR 07-APR-1997; 97US-00833504.

PA (GETH) GENENTECH INC.

PI Wells JA, Baca M, Presta LG;

DR WPI; 1998-594479/50.

XX New humanised antibody with specific alterations in human framework -
 PT specifically reactive with vascular endothelial growth factor, useful for
 PT inhibiting tumour growth.

PS Claim 3; Page 31; 45pp; English.

XX AAW6805 is the variable light region of the humanised A4.6.1 variant
 CC hu2.10. This variant is the consensus humanised clone obtained from phage
 CC sorting experiments. These antibodies are especially reactive with
 CC vascular endothelial growth factor (VEGF) and are used to inhibit growth
 CC of tumours by inhibiting mitogenic signalling
 CC

SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASODISNYLN 11
 |||||
 DB 24 SASODISNYLN 34

RESULT 9
 AAW70623
 ID AAW70623 standard; peptide; 107 AA.

AC AAW70623;

DT 27-JUN-1999 (first entry)

DE Humanised murine antibody A4.6.1 variant hu2.0 variable light domain.

XX light variable domain; murine; humanised antibody;
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 KW VEGF-induced angiogenesis; tumour; retinal disorder;
 KW age-related macular degeneration; diabetic retinopathy;
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
 XX

OS Synthetic.

OS Mus sp.

XX Homo sapiens.

XX WO9845331-A2.

XX 15-OCT-1998.

PF 03-APR-1998; 98WO-US006604.

XX 07-APR-1997; 97US-00833504.
PR 06-AUG-1997; 97US-00908469.
XX
XX (GETH) GENENTECH INC.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI WPI; 1998-568337/48.
XX
XX New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX
XX Example 2; Fig 5A; 100pp; English.
XX
XX The present sequence represents a variable light domain of the humanised
CC murine anti-vascular endothelial growth factor (anti-VEGF) antibody
CC variant hu2.0. The sequence is used in the course of the invention to
CC construct the humanised anti-VEGF antibody of the invention. The
CC humanised antibodies are used to inhibit VEGF-induced angiogenesis,
CC particularly for treating or preventing tumours (of any type) and retinal
CC disorders (e.g. age-related macular degeneration or diabetic
CC retinopathy). They can also be used to treat other conditions that
CC involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
CC atherosclerosis, Grave's disease, etc
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASODISNTLN 11
|||
Db 24 SASODISNTLN 34

RESULT 10
AAW70625
ID AAW70625 standard; peptide; 107 AA.

XX AAW70625;
AC
XX
XX 27-JAN-1999 (first entry)
DT
XX

DE Humanised murine antibody A4.6.1 variant hu2.10 variable light domain.

XX Light variable domain; murine; humanised antibody;
XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX VEGF-induced angiogenesis; tumour; retinal disorder;
XX age-related macular degeneration; diabetic retinopathy;
XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX

OS Synthetic.

OS Mus sp.

OS Homo sapiens.

XX W09845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-US006604.

XX 07-APR-1997; 97US-00833504.

XX 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.
XX

PT New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX
XX Example 2; Fig 5A; 100pp; English.
XX

XX The present sequence represents a variable light domain of the humanised
CC murine anti-vascular endothelial growth factor (anti-VEGF) antibody
CC variant hu2.10. The sequence is used in the course of the invention to
CC construct the humanised anti-VEGF antibody of the invention. The
CC humanised antibodies are used to inhibit VEGF-induced angiogenesis,
CC particularly for treating or preventing tumours (of any type) and retinal
CC disorders (e.g. age-related macular degeneration or diabetic
CC retinopathy). They can also be used to treat other conditions that
CC involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
CC atherosclerosis, Grave's disease, etc
XX

SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASODISNTLN 11
|||
Db 24 SASODISNTLN 34

RESULT 11
ABP61192
ID ABP61192 standard; protein; 107 AA.

XX ABP61192;
AC

XX 20-SEP-2002 (first entry)
DT

DE Humanised anti-VEGF antibody A4.6.1 variant variable light domain hu2.0.

XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
XX vascular endothelial growth factor; angiogenesis inhibitor; tumour;
XX retinal disorder; intraocular neovascular disorder; light chain;
XX variable domain.
XX

XX Homo sapiens.

OS Mus sp.

OS Synthetic.

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.

XX (WEL/) WELLS J A.

XX (PRE/) PRESTA L G.

XX (LOWM/) LOWMAN H B.

XX (CHEN/) CHEN Y M.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 2002-517920/55.

XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.
XX

XX Example 2; Fig 5; 47pp; English.

XX The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF

CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumour or a retinal disorder e.g. intraocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 5; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASODISNYLN 11
 |||||
 DB 24 SASODISNYLN 34

RESULT 12
 ABP61194
 ID ABP61194 standard; protein; 107 AA.
 XX
 AC ABP61194;

XX DT 20-SEP-2002 (first entry)

XX DE Humanised anti-VEGF antibody A4.6.1 variant variable light domain hu2.10.

XX KM Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KM vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KM retinal disorder; intraocular neovascular disorder; light chain;
 XX variable domain.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Synthetic.

XX PN US2002032315-A1.

XX PD 14-MAR-2002.

XX PF 06-APR-1998; 98US-00056160.

XX PR 06-AUG-1997; 97US-0054856P.

XX PA (BACA/) BACA M.
 PA (WELLS/) WELLS J A.
 PA (PRESTA/) PRESTA L G.
 PA (LOWMAN/) LOWMAN H B.
 PA (CHEN/) CHEN Y M.

XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX DR WPI; 2002-517920/55.

XX PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.

XX PS Example 2; Fig 5; 47pp; English.

XX CC The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumour or a retinal disorder e.g. intraocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 5; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASODISNYLN 11
 |||||
 DB 24 SASODISNYLN 34

RESULT 13
 AAW70620
 ID AAW70620 standard; peptide; 108 AA.
 XX
 AC AAW70620;

XX DT 27-JAN-1999 (first entry)

XX DE Anti-VEGF murine antibody A4.6.1 variable light domain.

XX KM light variable domain; murine; humanised antibody;
 KM anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 KM VEGF-induced angiogenesis; tumour; retinal disorder;
 KM age-related macular degeneration; diabetic retinopathy;
 KM rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX OS Mus sp.

XX PN WO9845331-A2.

XX PD 15-OCT-1998.

XX PF 03-APR-1998; 98WO-US006604.

XX PR 07-APR-1997; 97US-00835504.

XX PR 06-AUG-1997; 97US-00908469.

XX PA (GETH) GENENTECH INC.

XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX DR WPI; 1998-568337/48.

XX PT New humanised antibody with affinity for vascular endothelial growth
 PT factor - for treatment of tumours, retinal disease and other angiogenic
 PT states, also related nucleic acid, vectors and transformed cells.

XX PS Example 1; Fig 1B; 100pp; English.

XX CC The present sequence represents a variable light domain of the murine
 CC anti-vascular endothelial growth factor (anti-VEGF) antibody A4.6.1. The
 CC sequence is used to construct the humanised anti-VEGF antibody of the
 CC invention. The humanised antibodies are used to inhibit VEGF-induced
 CC angiogenesis, particularly for treating or preventing tumours (of any
 CC type) and retinal disorders (e.g. age-related macular degeneration or
 CC diabetic retinopathy). They can also be used to treat other conditions
 CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
 CC atherosclerosis, Grave's disease, etc

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASODISNYLN 11
 |||||
 DB 24 SASODISNYLN 34

RESULT 14
 AAW70618
 ID AAW70618 standard; peptide; 108 AA.
 XX
 AC AAW70618;

XX DT 27-JAN-1999 (first entry)

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XX Anti-VEGF humanised antibody F(ab)-12 variable light domain.
DE
XX
XX Light variable domain; murine; humanised antibody;
KM anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
KM VEGF-induced angiogenesis; tumour; retinal disorder;
KM age-related macular degeneration; diabetic retinopathy;
KM rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
XX Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
XX WO9845331-A2.
XX
XX 15-OCT-1998.
XX
XX 03-APR-1998; 98WO-US006604.
XX
XX 07-APR-1997; 97US-00833504.
XX 06-AUG-1997; 97US-00908469.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI WPI; 1998-568337/48.
XX
XX New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX
XX Claim 10; Fig 1B; 100pp; English.
XX
XX The present sequence represents a variable light domain of the humanised
CC anti-vascular endothelial growth factor (anti-VEGF) antibody F(ab)-12.
CC The sequence is used to construct the humanised anti-VEGF antibody of the
CC invention. The humanised antibodies are used to inhibit VEGF-induced
CC angiogenesis, particularly for treating or preventing tumours (of any
CC type) and retinal disorders (e.g. age-related macular degeneration or
CC diabetic retinopathy). They can also be used to treat other conditions
CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
CC atherosclerosis, Grave's disease, etc
XX
XX
SQ Sequence 108 AA;
Query Match 100.0%; Score 54; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASQDISNTYLN 11
DB 24 SASQDISNTYLN 34
RESULT 15
AAW70696
ID AAW70696 standard; peptide; 108 AA.
XX
XX AAW70696;
XX
XX 27-JAN-1999 (first entry)
XX
XX Anti-VEGF humanised antibody F(ab)-12 variable light domain.
XX
XX Light variable domain; murine; humanised antibody;
KM anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
KM VEGF-induced angiogenesis; tumour; retinal disorder;
KM age-related macular degeneration; diabetic retinopathy;
KM rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
XX Synthetic.
OS Mus sp.

```

```

OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 4
FT /note="Met or Leu"
XX
XX WO9845331-A2.
XX
XX 15-OCT-1998.
XX
XX 03-APR-1998; 98WO-US006604.
XX
XX 07-APR-1997; 97US-00833504.
XX 06-AUG-1997; 97US-00908469.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI WPI; 1998-568337/48.
XX
XX New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX
XX Claim 12; Page 4; 100pp; English.
XX
XX The present sequence represents a variable light domain of the humanised
CC anti-vascular endothelial growth factor (anti-VEGF) antibody. The
CC sequence is used to construct the humanised anti-VEGF antibody of the
CC invention. The humanised antibodies are used to inhibit VEGF-induced
CC angiogenesis, particularly for treating or preventing tumours (of any
CC type) and retinal disorders (e.g. age-related macular degeneration or
CC diabetic retinopathy). They can also be used to treat other conditions
CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
CC atherosclerosis, Grave's disease, etc
XX
XX
SQ Sequence 108 AA;
Query Match 100.0%; Score 54; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASQDISNTYLN 11
DB 24 SASQDISNTYLN 34
RESULT 16
AAB81988
ID AAB81988 standard; protein; 108 AA.
XX
XX AAB81988;
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KM cancer.
XX
XX Synthetic.
OS
XX WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
XX 30-SEP-1999; 99JP-00278291.
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX

```

```
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI WPI; 2001-266143/27.
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX
PS Claim 22; Page 172-173; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;

Query Match          100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNTYN 11
DB 24 SASQDISNTYN 34

RESULT 17
AAB81986
ID AAB81986 standard; protein; 108 AA.
XX
AC AAB81986;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.
XX
KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX
PS Example 1; Page 143-144; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;
```

```
Query Match          100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNTYN 11
DB 24 SASQDISNTYN 34

RESULT 18
AAB81990
ID AAB81990 standard; protein; 108 AA.
XX
AC AAB81990;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.
XX
KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
OS Mus musculus.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX
PS Claim 11; Page 174-175; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;

Query Match          100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNTYN 11
DB 24 SASQDISNTYN 34

RESULT 19
ABP61189
ID ABP61189 standard; protein; 108 AA.
XX
AC ABP61189;
XX
DT 20-SEP-2002 (first entry)
XX
DE Murine anti-VEGF mAbAVEGF A.4.6.1 antibody variable light domain.
```


XX CYCOSTATIC; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KM retinal disorder; intraocular neovascular disorder; murine; light chain;
 XX variable domain; mumabVEGF A.4.6.1.
 XX Mus sp.
 OS US2002032315-A1.
 PN 14-MAR-2002.
 PD 06-APR-1998; 98US-00056160.
 PF 06-APR-1998; 98US-00056160.
 PR 06-AUG-1997; 97US-0054856P.
 XX (BACA/) BACA M.
 PA (WELLS/) WELLS J A.
 PA (PRES/) PRESTA L G.
 PA (LOWM/) LOWMAN H B.
 PA (CHEN/) CHEN Y M.
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 DR WPI; 2002-517920/55.
 XX New humanised anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.
 PS Example 1; Fig 1; 47pp; English.
 XX The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumor or a retinal disorder e.g. intraocular
 CC neovascular disorders. The present sequence is the light chain variable
 CC domain of murine anti-VEGF mumabVEGF A.4.6.1 antibody, which was used to
 CC generate the humanised anti-VEGF antibodies of the invention
 XX Sequence 108 AA;
 SQ
 Query Match 100.0%; Score 54; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SASODISNTYN 11
 DB 24 SASODISNTYN 34
 RESULT 20
 ABP61265
 ID ABP61265 standard; protein; 108 AA.
 XX
 AC ABP61265;
 XX
 DT 20-SEP-2002 (first entry)
 XX
 DE Humanised anti-VEGF antibody variable light domain.
 XX
 KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KM vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KM retinal disorder; intraocular neovascular disorder; light chain;
 XX variable domain.
 XX Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 4

FT /label = Met, Leu
 XX US2002032315-A1.
 PN 14-MAR-2002.
 PD 06-APR-1998; 98US-00056160.
 PF 06-APR-1998; 98US-00056160.
 PR 06-AUG-1997; 97US-0054856P.
 XX (BACA/) BACA M.
 PA (WELLS/) WELLS J A.
 PA (PRES/) PRESTA L G.
 PA (LOWM/) LOWMAN H B.
 PA (CHEN/) CHEN Y M.
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 DR WPI; 2002-517920/55.
 XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.
 PS Claim 12; Page 31; 47pp; English.
 XX The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumor or a retinal disorder e.g. intraocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 XX Sequence 108 AA;
 SQ
 Query Match 100.0%; Score 54; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SASODISNTYN 11
 DB 24 SASODISNTYN 34
 RESULT 21
 ABP61187
 ID ABP61187 standard; protein; 108 AA.
 XX
 AC ABP61187;
 XX
 DT 20-SEP-2002 (first entry)
 XX
 DE Humanised anti-VEGF F(ab) (F(ab)-12) antibody variable light domain.
 XX
 KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KM vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KM retinal disorder; intraocular neovascular disorder; F(ab) (F(ab)-12);
 KM light chain; variable domain.
 XX Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 XX US2002032315-A1.
 PN 14-MAR-2002.
 PD 06-APR-1998; 98US-00056160.
 PF 06-APR-1998; 98US-00056160.
 PR 06-AUG-1997; 97US-0054856P.
 XX (BACA/) BACA M.

PA (WELL/) WELLS J A.
 PA (PRES/) PRESTA L G.
 PA (LOWM/) LOWMAN H B.
 PA (CHEN/) CHEN Y M.
 XX
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 XX
 DR WPI; 2002-517920/55.
 XX
 PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.
 XX
 PS Claim 10; Fig 1; 47pp; English.
 XX
 CC The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumour or a retinal disorder e.g. intraocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 XX
 SQ Sequence 108 AA;
 XX
 QY Query Match 100.0%; Score 54; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 SASQDISNTYLN 11
 24 SASQDISNTYLN 34
 XX
 RESULT 22
 ABU11011
 ID ABU11011 standard; protein; 108 AA.
 XX
 AC ABU11011;
 XX
 DT 04-FEB-2003 (first entry)
 XX
 DE Modified ganglioside GD3 antibody associated protein #4.
 XX
 KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 XX
 OS Synthetic.
 XX
 PS WO200278739-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 29-MAR-2002; 2002WO-JP003170.
 XX
 PR 29-MAR-2001; 2001JP-00097483.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Niwa R, Kanazawa J, Asada M;
 XX
 DR WPI; 2003-067410/06.
 XX
 PT Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX
 PS Claim 8; Page 100; 121pp; Japanese.
 XX
 CC The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic

CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 XX
 SQ Sequence 108 AA;
 XX
 QY Query Match 100.0%; Score 54; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 SASQDISNTYLN 11
 24 SASQDISNTYLN 34
 XX
 RESULT 23
 ABU11013
 ID ABU11013 standard; protein; 108 AA.
 XX
 AC ABU11013;
 XX
 DT 04-FEB-2003 (first entry)
 XX
 DE Modified ganglioside GD3 antibody associated protein #6.
 XX
 KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 XX
 OS Mus musculus.
 XX
 PS WO200278739-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 29-MAR-2002; 2002WO-JP003170.
 XX
 PR 29-MAR-2001; 2001JP-00097483.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Niwa R, Kanazawa J, Asada M;
 XX
 DR WPI; 2003-067410/06.
 XX
 PT Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX
 PS Claim 7; Page 113; 121pp; Japanese.
 XX
 CC The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 XX
 SQ Sequence 108 AA;
 XX
 QY Query Match 100.0%; Score 54; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 SASQDISNTYLN 11
 24 SASQDISNTYLN 34
 XX
 RESULT 24
 ADG31770
 ID ADG31770 standard; protein; 108 AA.
 XX

AC ADG31770;
XX 26-FEB-2004 (first entry)
XX V(L) domain of matured humanised murine anti-VEGF antibody SegID4.
DE protein library; in silico; VEGF; vascular endothelial growth factor;
XX antibody; computational prediction; V(H) domain; mouse; murine.
XX Synthetic.
OS Mus sp.
XX WO2003099999-A2.
XX 04-DEC-2003.
XX 20-MAY-2003; 2003WO-US016037.
XX 20-MAY-2002; 2002US-00153159.
XX 20-MAY-2002; 2002US-00153176.
XX (ABMA-) ABMAXIS INC.
XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S,
PI WPI; 2004-035117/03.
XX Constructing antibody libraries for generating protein libraries with
PT improved biological function comprising selecting from tester protein
PT sequences two peptide segments having 15% sequence identity with the lead
PT sequence.
XX Disclosure; SEQ ID NO 4; 354bp; English.
XX This invention relates to a novel method for the generation and screening
CC of a protein library in silico. Specifically, it refers to a high-
CC throughput method optimised for the identification of anti-VEGF (vascular
CC endothelial growth factor) antibodies with improved binding affinities
CC for their target antigen (VEGF), using computational prediction. The
CC present invention describes selecting proteins with a desirable function
CC based on their structural similarity to the target structural or
CC functional motif of a lead protein of interest. Accordingly, these
CC protein libraries are functionally biased with increased diversity so as
CC to increase the chance of identifying novel hits or combinations of
CC mutants with enhanced binding affinity. Furthermore, the sequence profile
CC based on the multiple structure alignment of the available lead structure
CC allows the sampling of a larger sequence space than by traditional
CC V(L) domain of affinity matured humanised murine anti-VEGF antibody, used
CC in an exemplification of the invention.
XX Sequence 108 AA;
SQ
Query Match 100.0%; Score 54; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34
RESULT 25
ADG31782
ID ADG31782 standard; protein; 108 AA.
XX ADG31782;
XX 26-FEB-2004 (first entry)
XX V(L) domain of the anti-VEGF two chain antibody AM2 protein SegID 16.
XX protein library; in silico; VEGF; vascular endothelial growth factor;
XX

KW antibody; computational prediction; V(H) domain; flexon; AM2;
XX two chain antibody; murine; mouse.
XX Synthetic.
OS Unidentified.
OS Mus sp.
XX WO2003099999-A2.
XX 04-DEC-2003.
XX 20-MAY-2003; 2003WO-US016037.
XX 20-MAY-2002; 2002US-00153159.
XX 20-MAY-2002; 2002US-00153176.
XX (ABMA-) ABMAXIS INC.
XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S,
PI WPI; 2004-035117/03.
XX N-PADB; ADG31781.
XX Constructing antibody libraries for generating protein libraries with
PT improved biological function comprising selecting from tester protein
PT sequences two peptide segments having 15% sequence identity with the lead
PT sequence.
XX Disclosure; SEQ ID NO 16; 354bp; English.
XX This invention relates to a novel method for the generation and screening
CC of a protein library in silico. Specifically, it refers to a high-
CC throughput method optimised for the identification of anti-VEGF (vascular
CC endothelial growth factor) antibodies with improved binding affinities
CC for their target antigen (VEGF), using computational prediction. The
CC present invention describes selecting proteins with a desirable function
CC based on their structural similarity to the target structural or
CC functional motif of a lead protein of interest. Accordingly, these
CC protein libraries are functionally biased with increased diversity so as
CC to increase the chance of identifying novel hits or combinations of
CC mutants with enhanced binding affinity. Furthermore, the sequence profile
CC based on the multiple structure alignment of the available lead structure
CC allows the sampling of a larger sequence space than by traditional
CC V(L) domain of the anti-VEGF two chain antibody AM2 protein, used in an
CC exemplification of the invention.
XX Sequence 108 AA;
SQ
Query Match 100.0%; Score 54; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34
RESULT 26
ADG31768
ID ADG31768 standard; protein; 108 AA.
XX ADG31768;
XX 26-FEB-2004 (first entry)
XX V(L) domain of parental humanised murine anti-VEGF antibody SegID2.
XX protein library; in silico; VEGF; vascular endothelial growth factor;
XX antibody; computational prediction; V(H) domain; mouse; murine.
XX Synthetic.
OS Mus sp.

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XX WO2003099999-A2.
XX
XX
XX 04-DEC-2003.
XX
XX 20-MAY-2003; 2003WO-US016037.
XX
XX 20-MAY-2002; 2002US-00153159.
XX 20-MAY-2002; 2002US-00153176.
XX
XX (ABMA-) ABMAXIS INC.
XX
XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;
XX WPI; 2004-035117/03.
XX
XX Constructing antibody libraries for generating protein libraries with
XX improved biological function comprising selecting from tester protein
XX sequences two peptide segments having 15% sequence identity with the lead
XX sequence.
XX
XX Disclosure; SEQ ID NO 2; 354pp; English.
XX
XX This invention relates to a novel method for the generation and screening
XX of a protein library in silico. Specifically, it refers to a high-
XX throughput method optimised for the identification of anti-VEGF (vascular
XX endothelial growth factor) antibodies with improved binding affinities
XX for their target antigen (VEGF), using computational prediction. The
XX present invention describes selecting proteins with a desirable function
XX based on their structural similarity to the target structural or
XX functional motif of a lead protein of interest. Accordingly, these
XX protein libraries are functionally biased with increased diversity so as
XX to increase the chance of identifying novel hits or combinations of
XX mutants with enhanced binding affinity. Furthermore, the sequence profile
XX based on the multiple structure alignment of the available lead structure
XX allows the sampling of a larger sequence space than by traditional,
XX multiple sequence alignment approaches. This polypeptide sequence is the
XX V(L) domain of parental humanised murine anti-VEGF antibody, used in an
XX exemplification of the invention.
XX
XX Sequence 108 AA;
SQ
XX
XX Query Match 100.0%; Score 54; DB 8; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 0.058;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SASODISNTYLN 11
DB 24 SASODISNTYLN 34
XX
XX RESULT 27
XX ADG31893
XX ID ADG31893 standard; peptide; 108 AA.
XX
XX AC ADG31893;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX V(L) protein sequence of various anti-VEGF antibodies SeqID 127.
XX
XX protein library; in silico; VEGF; vascular endothelial growth factor;
XX antibody; computational prediction; V(L) domain.
XX
XX Unidentified.
XX
XX WO2003099999-A2.
XX
XX 04-DEC-2003.
XX
XX 20-MAY-2003; 2003WO-US016037.
XX
XX 20-MAY-2002; 2002US-00153159.
XX
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```
PR 20-MAY-2002; 2002US-00153176.
XX
XX (ABMA-) ABMAXIS INC.
XX
XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;
XX WPI; 2004-035117/03.
XX
XX Constructing antibody libraries for generating protein libraries with
XX improved biological function comprising selecting from tester protein
XX sequences two peptide segments having 15% sequence identity with the lead
XX sequence.
XX
XX Disclosure; SEQ ID NO 127; 354pp; English.
XX
XX This invention relates to a novel method for the generation and screening
XX of a protein library in silico. Specifically, it refers to a high-
XX throughput method optimised for the identification of anti-VEGF (vascular
XX endothelial growth factor) antibodies with improved binding affinities
XX for their target antigen (VEGF), using computational prediction. The
XX present invention describes selecting proteins with a desirable function
XX based on their structural similarity to the target structural or
XX functional motif of a lead protein of interest. Accordingly, these
XX protein libraries are functionally biased with increased diversity so as
XX to increase the chance of identifying novel hits or combinations of
XX mutants with enhanced binding affinity. Furthermore, the sequence profile
XX based on the multiple structure alignment of the available lead structure
XX allows the sampling of a larger sequence space than by traditional,
XX multiple sequence alignment approaches. This polypeptide sequence is the
XX V(L) protein sequence of various anti-VEGF antibodies, used in an
XX exemplification of the invention.
XX
XX Sequence 108 AA;
SQ
XX
XX Query Match 100.0%; Score 54; DB 8; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 0.058;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SASODISNTYLN 11
DB 24 SASODISNTYLN 34
XX
XX RESULT 28
XX AAW70673
XX ID AAW70673 standard; peptide; 110 AA.
XX
XX AC AAW70673;
XX
XX DT 27-JAN-1999 (first entry)
XX
XX Anti-VEGF humanised antibody variable light domain of template MB1.6.
XX
XX light variable domain; murine; humanised antibody;
XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX VEGF-induced angiogenesis; tumour; retinal disorder;
XX age-related macular degeneration; diabetic retinopathy;
XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
XX Synthetic.
XX Mus sp.
XX OS Homo sapiens.
XX
XX PN WO9845331-A2.
XX
XX 15-OCT-1998.
XX
XX PD 03-APR-1998; 98WO-US006604.
XX
XX PF 07-APR-1997; 97US-00833504.
XX 06-AUG-1997; 97US-00908469.
XX
XX (GETH ) GENENTECH INC.
XX
```

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XX  Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI  WPI; 1998-568337/48.
XX
XX  New humanised antibody with affinity for vascular endothelial growth
PT  factor - for treatment of tumours, retinal disease and other angiogenic
XX  states, also related nucleic acid, vectors and transformed cells.
XX  Example 3; Fig 9A; 100pp; English.
XX
CC  The present sequence represents a variable light domain of the template
CC  molecule of the affinity-matured anti-vascular endothelial growth factor
CC  (anti-VEGF) antibody. The sequence is used in the course of the invention
CC  to produce the humanised anti-VEGF antibody of the invention. The
CC  humanised antibodies are used to inhibit VEGF-induced angiogenesis,
CC  particularly for treating or preventing tumours (of any type) and retinal
CC  disorders (e.g. age-related macular degeneration or diabetic
CC  retinopathy). They can also be used to treat other conditions that
CC  involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
CC  atherosclerosis, Grave's disease, etc
XX
SQ  Sequence 110 AA:
Query Match      100.0%; Score 54; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SASODISNTLN 11
    |||||
    24 SASODISNTLN 34

DB  27-JAN-1999 (first entry)

RESULT 29
AAW70677 standard; peptide; 110 AA.
XX
AC  AAW70677;
XX
DT  27-JAN-1999 (first entry)
XX
DE  Anti-VEGF humanised antibody variable light domain of variant Y0101.
XX
XX  Light variable domain; murine; humanised antibody;
XX  anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX  VEGF-induced angiogenesis; tumour; retinal disorder;
XX  age-related macular degeneration; diabetic retinopathy;
XX  rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
OS  Synthetic.
OS  Mus sp.
OS  Homo sapiens.
XX
XX  WO9845331-A2.
XX
XX  15-OCT-1998.
XX
XX  03-APR-1998; 98WO-US006604.
XX
XX  07-APR-1997; 97US-00833504.
XX
XX  06-AUG-1997; 97US-00908469.
XX
XX  (GETH ) GENENTECH INC.
XX
XX  Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX  WPI; 1998-568337/48.
XX
XX  New humanised antibody with affinity for vascular endothelial growth
PT  factor - for treatment of tumours, retinal disease and other angiogenic
PT  states, also related nucleic acid, vectors and transformed cells.
XX  Example 3; Fig 9A; 100pp; English.
XX

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```

XX  The present sequence represents a variable light domain of an affinity-
CC  matured anti-vascular endothelial growth factor (anti-VEGF) antibody
CC  variant. The sequence is used in the course of the invention to produce
CC  the humanised anti-VEGF antibody of the invention. The humanised
CC  antibodies are used to inhibit VEGF-induced angiogenesis, particularly
CC  for treating or preventing tumours (of any type) and retinal disorders
CC  (e.g. age-related macular degeneration or diabetic retinopathy). They can
CC  also be used to treat other conditions that involve angiogenesis, e.g.
CC  rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
XX
SQ  Sequence 110 AA:
Query Match      100.0%; Score 54; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SASODISNTLN 11
    |||||
    24 SASODISNTLN 34

DB  27-JAN-1999 (first entry)

RESULT 30
AAW70687 standard; peptide; 110 AA.
XX
AC  AAW70687;
XX
DT  27-JAN-1999 (first entry)
XX
DE  Anti-VEGF humanised antibody variable light domain of variant Y0317.
XX
XX  Light variable domain; murine; humanised antibody;
XX  anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX  VEGF-induced angiogenesis; tumour; retinal disorder;
XX  age-related macular degeneration; diabetic retinopathy;
XX  rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
OS  Synthetic.
OS  Mus sp.
OS  Homo sapiens.
XX
XX  WO9845331-A2.
XX
XX  15-OCT-1998.
XX
XX  03-APR-1998; 98WO-US006604.
XX
XX  07-APR-1997; 97US-00833504.
XX
XX  06-AUG-1997; 97US-00908469.
XX
XX  (GETH ) GENENTECH INC.
XX
XX  Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX  WPI; 1998-568337/48.
XX
XX  New humanised antibody with affinity for vascular endothelial growth
PT  factor - for treatment of tumours, retinal disease and other angiogenic
PT  states, also related nucleic acid, vectors and transformed cells.
XX  Claim 27; Fig 10A; 100pp; English.
XX
CC  The present sequence represents a variable light domain of an affinity-
CC  matured anti-vascular endothelial growth factor (anti-VEGF) antibody
CC  variant. The sequence is used in the course of the invention to produce
CC  the humanised anti-VEGF antibody of the invention. The humanised
CC  antibodies are used to inhibit VEGF-induced angiogenesis, particularly
CC  for treating or preventing tumours (of any type) and retinal disorders
CC  (e.g. age-related macular degeneration or diabetic retinopathy). They can
CC  also be used to treat other conditions that involve angiogenesis, e.g.
CC  rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
XX

```

SQ Sequence 110 AA;

Query Match 100.0%; Score 54; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34

RESULT 31
AAW70675
ID AAW70675 standard; peptide; 110 AA.

AC AAW70675;

DT 27-JAN-1999 (first entry)

DE Anti-VEGF humanised antibody variable light domain of variant H2305.6.

XX Light variable domain; murine; humanised antibody;

XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;

XX VEGF-induced angiogenesis; tumour; retinal disorder;

XX age-related macular degeneration; diabetic retinopathy;

XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX Synthetic.

OS Mus sp.

OS Homo sapiens.

XX W09845331-A2.

XX 15-OCT-1998.

PF 03-APR-1998; 98WO-US006604.

XX 07-APR-1997; 97US-00833504.

PR 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

DR WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth
factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.

XX Example 3; Fig 9A; 100pp; English.

XX The present sequence represents a variable light domain of an affinity-
matured anti-vascular endothelial growth factor (anti-VEGF) antibody
CC variant. The sequence is used in the course of the invention to produce
CC the humanised anti-VEGF antibody of the invention. The humanised
CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
CC for treating or preventing tumours (of any type) and retinal disorders
CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
CC also be used to treat other conditions that involve angiogenesis, e.g.
CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

XX Sequence 110 AA;

Query Match 100.0%; Score 54; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34

RESULT 32

ID AAB05897

AC AAB05897;

DT 17-OCT-2000 (first entry)

DE Humanised anti-VEGF antibody F(ab)-12 light chain variable domain.

XX Humanised; F(ab)-12; light chain variable domain; antibody variant;

XX phage display; randomised library; cytosolic; antiarthritis;

XX anti-psoriatic; antidiabetic; antiinflammatory; antiarteriosclerotic;

XX vascular endothelial growth factor; VEGF; breast cancer; lung cancer;

XX retinoblastoma; rheumatoid arthritis; psoriasis; atherosclerosis;

XX diabetic retinopathy; complementarity determining region; CDR.

XX Homo sapiens.

OS Synthetic.

PN W0200029584-A1.

PD 25-MAY-2000.

PF 16-NOV-1999; 99WO-US027153.

PR 18-NOV-1998; 98US-0108945P.

XX (GETH) GENENTECH INC.

PI Chen YM, Lowman HB, Muller Y;

DR WPI; 2000-387797/33.

XX Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.

PS Disclosure; Fig 1A; 110pp; English.

XX The present sequence is the light chain variable domain of F(ab)-12, a
CC humanised anti-vascular endothelial growth factor (VEGF) antibody. F(ab)-
CC 12 was the parent antibody used in the production of a large number of
CC antibody variants containing randomised peptide inserts within the
CC complementarity determining regions (CDRs). Phage display libraries were
CC subjected to eight rounds of selection to isolate variants with an
CC antigen binding affinity at least two-fold stronger than the binding
CC affinity of parent antibody for the target VEGF antibody. The anti-VEGF
CC antibody variants may be useful in diagnostic assays for detecting in
CC expression of VEGF in cells, tissue or serum. They may also be used in
CC the prevention and treatment of neoplastic diseases such as breast
CC cancer, lung cancer and retinoblastoma, and non-neoplastic diseases
CC including rheumatoid arthritis, psoriasis, atherosclerosis, and diabetic
CC and other proliferative retinopathies

XX Sequence 110 AA;

Query Match 100.0%; Score 54; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34

RESULT 33

AAB13380

ID AAB13380 standard; protein; 110 AA.

XX AAB13380;

DT 21-NOV-2000 (first entry)
XX Anti-VEGF antibody Y0317 light chain variable domain.
XX
XX Y0317; vascular endothelial cell growth factor; VEGF; antibody;
XX antiinflammatory; cerebroprotective; cytosolic; antirheumatic;
XX antiarthritic; antiporiatic; antiarteriosclerotic; antidiabetic;
XX antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
XX psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
XX neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
XX tissue transplantation; inflammation; oedema; trauma;
XX complementarity determining region; CDR.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Region 24..33
XX /label= CDR-L1
XX Region 50..56
XX /label= CDR-L2
XX Region 89..97
XX /label= CDR-L3
XX
XX WO200037502-A2.
XX
XX 29-JUN-2000.
XX
XX 09-DEC-1999; 99WO-US029475.
XX
XX 22-DEC-1998; 98US-00218481.
XX
XX (GETH) GENENTECH INC.
XX
XX Van Bruggen N, Ferrara N;
XX
XX WPI: 2000-442646/38.
XX
XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
XX diabetes and chronic inflammation in a mammal, comprises administering a
XX human vascular endothelial cell growth factor antagonist.
XX
XX Disclosure; Fig 14A; 60pp; English.
XX
XX The present sequence is the light chain variable region of the affinity
XX matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody
XX Y0317. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
XX be used to treat conditions characterised by undesirable excessive
XX neovascularisation. Such conditions include tumors (especially solid
XX ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
XX other retinopathies, retrolental fibroplasia, age-related macular
XX degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
XX (including Grave's disease), corneal and other tissue transplantation,
XX and chronic inflammation. Oedemas associated with tumors, strokes and
XX head trauma, and ascites associated with malignancies, meigs's syndrome,
XX lung inflammation, nephrotic syndrome, pericardial effusion and pleural
XX effusion, may also be treated. Monoclonal antibodies are generated in
XX hybridoma cells and those with affinity for VEGF are identified by
XX immunoprecipitation or by an in vitro binding assay
XX
XX Sequence 110 AA;
XX
XX Query Match 100.0%; Score 54; DB 3; Length 110;
XX Best Local Similarity 100.0%; Pred. No. 0.059;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 SASQDISNYLN 11
XX |||||
XX |||||
XX |||||
XX |||||
XX 24 SASQDISNYLN 34
XX
XX RESULT 34
XX AAB13376
XX ID AAB13376 standard; protein; 110 AA.

XX AAB13376;
XX
XX 12-SEP-2003 (revised)
XX 21-NOV-2000 (first entry)
XX F(ab)-12 anti-VEGF antibody light chain variable domain.
XX
XX Humanised; F(ab)-12; vascular endothelial cell growth factor; VEGF;
XX antiinflammatory; cerebroprotective; cytosolic; antirheumatic;
XX antiarthritic; antiporiatic; antiarteriosclerotic; antidiabetic;
XX antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
XX psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
XX neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
XX tissue transplantation; inflammation; oedema; trauma;
XX complementarity determining region; CDR.
XX
XX Homo sapiens.
XX Mus sp.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX Region 24..34
XX /label= CDR-L1
XX Region 50..56
XX /label= CDR-L2
XX Region 89..97
XX /label= CDR-L3
XX
XX WO200037502-A2.
XX
XX 29-JUN-2000.
XX
XX 09-DEC-1999; 99WO-US029475.
XX
XX 22-DEC-1998; 98US-00218481.
XX
XX (GETH) GENENTECH INC.
XX
XX Van Bruggen N, Ferrara N;
XX
XX WPI: 2000-442646/38.
XX
XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
XX diabetes and chronic inflammation in a mammal, comprises administering a
XX human vascular endothelial cell growth factor antagonist.
XX
XX Disclosure; Fig 14A; 60pp; English.
XX
XX The present sequence is the light chain variable domain of humanised anti-
XX vascular endothelial cell growth factor (anti-VEGF) antibody F(ab)-12.
XX It may be used to treat conditions characterised by undesirable excessive
XX neovascularisation. Such conditions include tumors (especially solid
XX ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
XX other retinopathies, retrolental fibroplasia, age-related macular
XX degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
XX (including Grave's disease), corneal and other tissue transplantation,
XX and chronic inflammation. Oedemas associated with tumors, strokes and
XX head trauma, and ascites associated with malignancies, meigs's syndrome,
XX lung inflammation, nephrotic syndrome, pericardial effusion and pleural
XX effusion, may also be treated. Affinity matured anti-VEGF antibodies are
XX also used as therapeutic agents. Monoclonal antibodies are generated in
XX hybridoma cells and those with affinity for VEGF are identified by
XX immunoprecipitation or by an in vitro binding assay. (Updated on 12-SEP-
XX 2003 to standardise OS field)
XX
XX Sequence 110 AA;
XX
XX Query Match 100.0%; Score 54; DB 3; Length 110;
XX Best Local Similarity 100.0%; Pred. No. 0.059;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 SASQDISNYLN 11

DB 24 SASQDISNTYLN 34

RESULT 35

ABP61242 ID ABP61242 standard; protein; 110 AA.

AC ABP61242;

DT 20-SEP-2002 (first entry)

DE Humanised anti-VEGF MB1.6 antibody variable light domain.

KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;

KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;

KW retinal disorder; intraocular neovascular disorder; MB1.6; light chain;

XX variable domain.

OS Homo sapiens.

OS Mus sp.

OS Synthetic.

XX Key

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

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FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

RESULT 36

ABP61256 ID ABP61256 standard; protein; 110 AA.

AC ABP61256;

DT 20-SEP-2002 (first entry)

DE Humanised anti-VEGF Y0317 antibody variable light domain.

KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;

KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;

KW retinal disorder; intraocular neovascular disorder; Y0317; light chain;

XX variable domain.

OS Homo sapiens.

OS Mus sp.

OS Synthetic.

XX Key

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

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FT Domain

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FT Domain

FT Domain

FT Domain

RESULT 37

ABP61244 ID ABP61244 standard; protein; 110 AA.

AC ABP61244;

DT 20-SEP-2002 (first entry)

DE Humanised anti-VEGF Y0317 antibody variable light domain.

KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;

KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;

KW retinal disorder; intraocular neovascular disorder; Y0317; light chain;

XX variable domain.

OS Homo sapiens.

OS Mus sp.

OS Synthetic.

XX Key

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

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FT Domain

FT Domain


```
ID ABP61244 standard; protein; 110 AA.
XX
AC ABP61244;
XX
DT 20-SEP-2002 (first entry)
XX
DE Humanised anti-VEGF H2305.6 antibody variable light domain.
XX
DE Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
XX KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
XX KW retinal disorder; intraocular neovascular disorder; H2305.6; light chain;
XX KW variable domain.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Domain 24..34
FT /label= CDR-L1
FT 50..57
FT /label= CDR-L2
FT 89..97
FT Domain /label= CDR-L3
XX
PN US2002032315-A1.
XX
PD 14-MAR-2002.
XX
PF 06-APR-1998; 98US-00056160.
XX
PR 06-AUG-1997; 97US-0054856P.
XX
PA (BACA/) BACA M.
PA (WELL/) WELLS J A.
PA (PRES/) PRESTA L G.
PA (LOWM/) LOWMAN H B.
PA (CHEN/) CHEN Y M.
XX
PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX
DR WPI; 2002-517920/55.
XX
PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.
XX
PS Example 3; Fig 9; 47pp; English.
XX
CC The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
CC particularly those having a tumour or a retinal disorder e.g. intraocular
CC neovascular disorders. The present sequence is an exemplary light chain
CC variable domain of the humanised anti-VEGF antibody of the invention
XX
SQ Sequence 110 AA;
XX
Query Match 100.0%; Score 54; DB 5; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASQDISNTNLTN 11
DB 24 SASQDISNTNLTN 34
XX
RESULT 38
ID ABP61246 standard; protein; 110 AA.
XX
AC ABP61246;
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```
XX
DT 20-SEP-2002 (first entry)
XX
DE Humanised anti-VEGF Y0101 antibody variable light domain.
XX
DE Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
XX KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
XX KW retinal disorder; intraocular neovascular disorder; Y0101; light chain;
XX KW variable domain.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Domain 24..34
FT /label= CDR-L1
FT 50..57
FT /label= CDR-L2
FT 89..97
FT Domain /label= CDR-L3
XX
PN US2002032315-A1.
XX
PD 14-MAR-2002.
XX
PF 06-APR-1998; 98US-00056160.
XX
PR 06-AUG-1997; 97US-0054856P.
XX
PA (BACA/) BACA M.
PA (WELL/) WELLS J A.
PA (PRES/) PRESTA L G.
PA (LOWM/) LOWMAN H B.
PA (CHEN/) CHEN Y M.
XX
PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX
DR WPI; 2002-517920/55.
XX
PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.
XX
PS Example 3; Fig 9; 47pp; English.
XX
CC The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
CC particularly those having a tumour or a retinal disorder e.g. intraocular
CC neovascular disorders. The present sequence is an exemplary light chain
CC variable domain of the humanised anti-VEGF antibody of the invention
XX
SQ Sequence 110 AA;
XX
Query Match 100.0%; Score 54; DB 5; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASQDISNTNLTN 11
DB 24 SASQDISNTNLTN 34
XX
RESULT 39
ID AAR33257 standard; protein; 128 AA.
XX
AC AAR33257;
XX
DT 25-MAR-2003 (revised)
DT 12-JUL-1993 (first entry)
```

```

XX DE Rat immunoglobulin L chain variable region of pKM641IA2.
XX XX Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
XX KW humanised; chimeric; antibody; expression vector.
XX OS Rattus rattus.
XX XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..20
XX FT Protein /note="Signal peptide"
XX FT /note="Mature protein"
XX PN EP53199-A2.
XX PD 24-MAR-1993.
XX PF 18-SEP-1992; 92EP-00116026.
XX PR 18-SEP-1991; 91JP-00238375.
XX PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.
XX PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX XX WPI; 1993-095510/12.
XX DR N-PSDB; AAQ33258.
XX PT Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
XX PT cancers, such as melanoma, neuroblastoma, etc.
XX PS Claim 6; Page 30-31; 63pp; English.
XX XX
XX CC The sequences given in AAR33256-57 represent rat heavy and light chain
XX CC variable regions respectively. The DNA sequences encoding these proteins
XX CC were used in the construction of humanised chimeric antibody expression
XX CC vectors. In these humanised antibodies none of the amino acids of the non
XX CC -human animal Ab variable region have been changed. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
XX SQ Sequence 128 AA;
XX
XX Query Match 100.0%; Score 54; DB 2; Length 128;
XX Best Local Similarity 100.0%; Pred. No. 0.071;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASODISNTLN 11
Db 44 SASODISNTLN 54

```

RESULT 40
AAR53340
ID AAR53340 standard; protein; 128 AA.
XX
AC AAR53340;
XX
DT 18-NOV-1994 (first entry)
XX
DE KM641 H chain variable region.
XX
KW Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
KW expression vector; heavy; light; chain; hypervariable region; CDR;
KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label=sig_peptide
XX
PN AU9346181-A.

```

XX XX 17-MAR-1994.
XX PD
XX PF 07-SEP-1993; 93AU-00046181.
XX PR 07-SEP-1992; 92JP-00238452.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
XX DR WPI; 1994-126857/16.
XX DR N-PSDB; AAQ5438.
XX PT Humanised antibody specific for ganglioside GM2 - used for producing a
XX PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX PS Example 2; Page 115-116; 191pp; English.
XX CC
XX CC Example 2 describes the construction of the vector pCh1641HA1 for
XX CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3
XX CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
XX CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
XX CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641IA2) are given in
XX CC AAQ5438-39. A KM641-derived chimeric human Ab H chain expression vector
XX CC was constructed by joining the H chain variable region gene from
XX CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the
XX CC synthetic DNAs given in AAQ5439 and AAQ5440
XX SQ Sequence 128 AA;
XX
XX Query Match 100.0%; Score 54; DB 2; Length 128;
XX Best Local Similarity 100.0%; Pred. No. 0.071;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASODISNTLN 11
Db 44 SASODISNTLN 54

```

Search completed: December 17, 2004, 18:29:03
Job time : 34.4326 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 17, 2004, 18:13:27 ; Search time 6.67416 Seconds
(without alignments)
109.302 Million cell updates/sec

Title: US-10-089-500-6
Perfect score: 54
Sequence: 1 SASQDISNYLN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	110	4	US-09-440-781-94
2	54	100.0	128	4	US-09-225-322B-10
3	54	100.0	128	4	US-09-225-322B-19
4	54	100.0	128	4	US-09-764-304-10
5	54	100.0	128	4	US-09-764-304-19
6	51	94.4	109	4	US-09-386-658A-4
7	50	92.6	11	2	US-08-480-434-76
8	50	92.6	11	2	US-08-053-451B-76
9	50	92.6	11	3	US-08-649-100-11
10	50	92.6	11	3	US-08-649-100-27
11	50	92.6	31	3	US-08-525-539A-5
12	50	92.6	76	3	US-08-851-362D-20
13	50	92.6	105	3	US-08-851-362D-28
14	50	92.6	105	3	US-08-851-362D-34
15	50	92.6	105	3	US-08-851-362D-38
16	50	92.6	107	2	US-08-480-434-74
17	50	92.6	107	2	US-08-053-451B-74
18	50	92.6	107	2	US-08-053-451B-176
19	50	92.6	108	3	US-09-065-059-3
20	50	92.6	109	1	US-07-942-245-10
21	50	92.6	127	1	US-08-137-117D-37
22	50	92.6	127	1	US-08-436-717-37
23	50	92.6	127	3	US-08-649-100-17
24	50	92.6	127	3	US-08-649-100-33
25	50	92.6	131	1	US-08-236-520-2
26	50	92.6	131	5	PCT-US95-05262-2
27	50	92.6	273	2	US-08-403-853-18

28	49	90.7	112	3	US-08-487-761-13	Sequence 13, Appl
29	47	87.0	105	3	US-08-851-362D-24	Sequence 24, Appl
30	47	87.0	107	1	US-08-458-516-8	Sequence 8, Appl
31	47	87.0	107	1	US-08-458-516-9	Sequence 9, Appl
32	47	87.0	107	2	US-08-652-558-2	Sequence 2, Appl
33	47	87.0	107	2	US-08-652-558-35	Sequence 35, Appl
34	47	87.0	107	3	US-09-254-189-1	Sequence 1, Appl
35	47	87.0	109	2	US-07-934-373C-47	Sequence 47, Appl
36	47	87.0	109	3	US-08-437-642B-47	Sequence 47, Appl
37	47	87.0	127	1	US-08-458-516-5	Sequence 5, Appl
38	47	87.0	127	3	US-08-348-548-4	Sequence 4, Appl
39	47	87.0	127	5	PCT-US95-15716-4	Sequence 4, Appl
40	47	87.0	214	1	US-08-425-763-1	Sequence 1, Appl
41	47	87.0	214	1	US-08-458-516-12	Sequence 12, Appl
42	47	87.0	214	2	US-07-934-373C-24	Sequence 24, Appl
43	47	87.0	214	2	US-07-934-373C-39	Sequence 39, Appl
44	47	87.0	214	2	US-07-934-373C-40	Sequence 40, Appl
45	47	87.0	214	2	US-08-788-800-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-09-440-781-94
; Sequence 94, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 94
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match      100.0%; Score 54; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 2
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17

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/ PRIOR APPLICATION NUMBER: US07/947,674
/ PRIOR FILING DATE: 1992-09-17
/ PRIOR APPLICATION NUMBER: JP 3-238375
/ PRIOR FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-09-225-322B-10

Query Match          100.0%; Score 54; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASQDISNYLN 11
        |||||
        44 SASQDISNYLN 54

RESULT 3
US-09-225-322B-19
/ Sequence 19, Application US/09225322B
/ Patent No. 6437098
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/225,322B
/ CURRENT FILING DATE: 1999-01-05
/ PRIOR APPLICATION NUMBER: US 08/454,680
/ PRIOR FILING DATE: 1995-05-31
/ PRIOR APPLICATION NUMBER: US 08/408,133
/ PRIOR FILING DATE: 1995-03-21
/ PRIOR APPLICATION NUMBER: US 08/292,178
/ PRIOR FILING DATE: 1994-08-17
/ PRIOR APPLICATION NUMBER: US07/947,674
/ PRIOR FILING DATE: 1992-09-17
/ PRIOR APPLICATION NUMBER: JP 3-238375
/ PRIOR FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: light chain
US-09-225-322B-19

Query Match          100.0%; Score 54; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASQDISNYLN 11
        |||||
        44 SASQDISNYLN 54

RESULT 4
US-09-764-304-10
/ Sequence 10, Application US/09764304
/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain
```

```
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain

Query Match          100.0%; Score 54; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASQDISNYLN 11
        |||||
        44 SASQDISNYLN 54

RESULT 5
US-09-764-304-19
/ Sequence 19, Application US/09764304
/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain
```

OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 100.0%; Score 54; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.024; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
|||||
DB 44 SASODISNYLN 54

RESULT 6
US-09-386-658A-4

Sequence 4, Application US/0938658A
Patent No. 6593137
GENERAL INFORMATION:
APPLICANT: Erlanger, Bernard F.
APPLICANT: Chen, Bi-Xing
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
FILE REFERENCE: 0575/54182
CURRENT APPLICATION NUMBER: US/09/386,658A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 4
LENGTH: 109
TYPE: PRT
ORGANISM: Mouse
US-09-386-658A-4

Query Match 94.4%; Score 51; DB 4; Length 109;
Best Local Similarity 90.9%; Pred. No. 0.067; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
|||||
DB 24 SASODISNYLN 34

RESULT 7
US-08-480-434-76

Sequence 76, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Dillow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 76:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-434-76

Query Match 92.6%; Score 50; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0076; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
|||||
DB 2 ASODISNYLN 11

RESULT 8
US-08-053-451B-76

Sequence 76, Application US/08053451B
Patent No. 595584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Dillow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-76

Query Match 92.6%; Score 50; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0076; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
|||||
DB 2 ASODISNYLN 11

RESULT 9
US-08-649-100-11
Sequence 11, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUSE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO. MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESSES:
ADDRESSER: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
ZIP: 22040-0747
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-11

Query Match 92.6%; Score 50; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 2 ASODISNYLN 11

RESULT 10
US-08-649-100-27
Sequence 27, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUSE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO. MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESSES:
ADDRESSER: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH

STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-27

Query Match 92.6%; Score 50; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 2 ASODISNYLN 11

RESULT 11
US-08-525-539A-5
Sequence 5, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MC3 ANTI-BB46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESSES:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
ZIP: 94304-1018
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 31 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-525-539A-5

Query Match 92.6%; Score 50; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 12 ASQDISNYLN 21

RESULT 12
US-08-851-362D-20
; Sequence 20, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-08-851-362D-20

Query Match 92.6%; Score 50; DB 3; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 6 ASQDISNYLN 15

RESULT 13
US-08-851-362D-28
; Sequence 28, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 105
; TYPE: PRT
; ORGANISM: human
US-08-851-362D-28

Query Match 92.6%; Score 50; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 6 ASQDISNYLN 15

RESULT 14
US-08-851-362D-34
; Sequence 34, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 105
; TYPE: PRT
; ORGANISM: human
US-08-851-362D-34

Query Match 92.6%; Score 50; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 6 ASQDISNYLN 15

RESULT 15
US-08-851-362D-38
; Sequence 38, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 105
; TYPE: PRT
; ORGANISM: human
US-08-851-362D-38

Query Match 92.6%; Score 50; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 6 ASQDISNYLN 15

RESULT 16
US-08-480-434-74
; Sequence 74, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:

APPLICANT: Charles C. Dittlow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3694
TELEFAX: (415) 854-3660
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: N
ANTI-SENSE: N
US-08-480-434-74

Query Match 92.6%; Score 50; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 25 ASQDISNYLN 34

RESULT 17
US-08-053-451B-74
Sequence 74, Application US/08053451B
Patent No. 5955584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Dittlow, Charles C.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B

FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHEICAL: N
ANTI-SENSE: N
US-08-053-451B-74

Query Match 92.6%; Score 50; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 25 ASQDISNYLN 34

RESULT 18
US-08-053-451B-176
Sequence 176, Application US/08053451B
Patent No. 5955584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Dittlow, Charles C.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-053-451B-176

Query Match 92.6%; Score 50; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.099; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 25 ASODISNYLN 34

RESULT 19
US-09-065-059-3
Sequence 3, Application US/09065059
Patent No. 6068841

GENERAL INFORMATION:
APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-518-5100
TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-065-059-3

Query Match 92.6%; Score 50; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 25 ASODISNYLN 34

RESULT 20
US-07-942-245-10
Sequence 10, Application US/07942245
Patent No. 5639641

GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.

TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-10

Query Match 92.6%; Score 50; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 25 ASODISNYLN 34

RESULT 21
US-08-137-117D-37
Sequence 37, Application US/08137117D
Patent No. 5795965

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-37

Query Match 92.6%; Score 50; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
|||||
DB 45 ASODISNYLN 54

RESULT 22
US-08-436-717-37
Sequence 37, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masaaki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/126/AOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-37

Query Match 92.6%; Score 50; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
|||||
DB 45 ASODISNYLN 54

RESULT 23
US-08-649-100-17
Sequence 17, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-17

Query Match 92.6%; Score 50; DB 3; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
|||||

Db 45 ASODISNYLN 54

RESULT 24

US-08-649-100-33

Sequence 33, Application US/08649100
Patent No. 6114507

GENERAL INFORMATION:

APPLICANT: SHIRAKAWA, KAMON

APPLICANT: MATSUBE, TOMOKAZU

APPLICANT: NAGATA, SHIGEKAZU

APPLICANT: CO, MAN SONG

APPLICANT: VASQUEZ, MAXIMILIANO

TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY

TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESSES: 41

ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH

STREET: PO BOX 747

CITY: FALLS CHURCH

STATE: VA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/649,100

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY JR, GERALD M

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1110-160

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 127 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-649-100-33

Query Match 92.6%; Score 50; DB 3; Length 127;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 45 ASODISNYLN 54

RESULT 25
US-08-236-520-2
Sequence 2, Application US/08236520
Patent No. 5591629

GENERAL INFORMATION:

APPLICANT: Rodriguez, Moses

APPLICANT: Miller, David J.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE

TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.

STREET: Two Millitta Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/236,520

FILING DATE: 29-APR-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 27,227

REFERENCE/DOCKET NUMBER: MM92-01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 131 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-236-520-2

Query Match 92.6%; Score 50; DB 1; Length 131;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 45 ASODISNYLN 54

RESULT 26
PCT-US95-05262-2
Sequence 2, Application PC/TUS9505262

GENERAL INFORMATION:

APPLICANT: Mayo Foundation for Medical Education Research

TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE

TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.

STREET: Two Millitta Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05262

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/236,520

FILING DATE: April 29, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 27,227

REFERENCE/DOCKET NUMBER: MM92-01 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 131 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US95-05262-2

Query Match 92.6%; Score 50; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
|||||
Db 45 ASODISNYLN 54

RESULT 27

US-08-403-853-18
Sequence 18, Application US/08403853
Patent No. 584094
GENERAL INFORMATION:
APPLICANT: HUDSON, Peter J.
APPLICANT: LAH, Maria
APPLICANT: KORRT, Alex A.
APPLICANT: IRVING, Robert A.
APPLICANT: ATWELL, John L.
APPLICANT: MALBY, Robyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA: AU PL 4973
APPLICATION NUMBER: 25-SEP-1992
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-853-18

Query Match 92.6%; Score 50; DB 2; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
|||||
Db 183 ASODISNYLN 192

RESULT 28

US-08-487-761-13
Sequence 13, Application US/08487761
Patent No. 6217866
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Givoli, David
APPLICANT: Bellot, Francoise
APPLICANT: Kris, Richard
APPLICANT: Ricca, George A.
APPLICANT: Cheadle, Christopher
APPLICANT: South, Victoria J.
TITLE OF INVENTION: Monoclonal Antibodies Specific to Human
TITLE OF INVENTION: Epidermal Growth Factor Receptor and Therapeutic Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,761
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,411
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A0207C-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3817
TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-761-13

Query Match 90.7%; Score 49; DB 3; Length 112;
Best Local Similarity 90.9%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
|||||
Db 24 SASODIRNYLN 34

RESULT 29

US-08-851-362D-24
Sequence 24, Application US/08851362D
Patent No. 6235883
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
TITLE OF INVENTION: Growth Factor Receptor
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D

;; CURRENT FILING DATE: 1997-05-05
;; NUMBER OF SEQ ID NOS: 49
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 24
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: human
US-08-851-362D-24

Query Match 87.0%; Score 47; DB 3; Length 105;
Best Local Similarity 90.0%; Pred. No. 0.33;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
||||:||||
DB 6 ASQDINNYLN 15

RESULT 30
US-08-458-516-8
; Sequence 8, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2422
; TELEFAX: 415-326-2400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-8

Query Match 87.0%; Score 47; DB 1; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.34;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
||||:||||
DB 25 ASQDINNYLN 34

RESULT 31
US-08-458-516-9

;; Sequence 9, Application US/08458516
;; Patent No. 5777085
;; GENERAL INFORMATION:
;; APPLICANT: Co, Man Sung
;; APPLICANT: Tso, J. Yun
;; TITLE OF INVENTION: Humanized Antibodies Reactive with
;; TITLE OF INVENTION: GPIIB/IIIA
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSES: William M. Smith
;; STREET: One Market Plaza, Steuart Tower, Suite 2000
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-9

Query Match 87.0%; Score 47; DB 1; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.34;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
||||:||||
DB 25 ASQDINNYLN 34

RESULT 32
US-08-652-558-2
; Sequence 2, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
; APPLICANT: LIN, AUGUSTINE YEE-THAN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: BANNER & WITCOFF
; STREET: 75 STATE STREET, 23RD FLOOR
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-2

Query Match 87.0%; Score 47; DB 2; Length 107;
Best Local Similarity 90.9%; Pred. No. 0.34;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
DB 24 SASQGISNYLN 34

RESULT 33
US-08-652-558-35
Sequence 35, Application US/08652558
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-35

Query Match 87.0%; Score 47; DB 2; Length 107;
Best Local Similarity 90.9%; Pred. No. 0.34;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
DB 24 SASQGISNYLN 34

RESULT 34
US-09-254-189-1
Sequence 1, Application US/09254189
Patent No. 6150792
GENERAL INFORMATION:
APPLICANT: Lundquist, Tomas
TITLE OF INVENTION: Sequence Listing
Patent No. 6150792
FILE REFERENCE: 3526/00000
CURRENT APPLICATION NUMBER: US/09/254,189
CURRENT FILING DATE: 1999-03-02
EARLIER APPLICATION NUMBER: 00/000,000
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:humanized
US-09-254-189-1

Query Match 87.0%; Score 47; DB 3; Length 107;
Best Local Similarity 90.9%; Pred. No. 0.34;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
DB 24 SASQGISNYLN 34

RESULT 35
US-07-934-373C-47
Sequence 47, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-47

Query Match 87.0%; Score 47; DB 2; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.34;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 25 ASODINNYLN 34

RESULT 36
US-08-437-642B-47
Sequence 47, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Prestea
TITLE OF INVENTION: Immunoglobulin variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: 08/146206
APPLICATION NUMBER: 17-NOV-1993
PRIOR APPLICATION DATA: PCT/US92/05126
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-47

Query Match 87.0%; Score 47; DB 3; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.34;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 25 ASODINNYLN 34

RESULT 37
US-08-458-516-5
Sequence 5, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co. Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-5

Query Match 87.0%; Score 47; DB 1; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.41;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 45 ASODINNYLN 54

RESULT 38
US-08-348-548-4
Sequence 4, Application US/08348548
Patent No. 6258529
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson
;; STREET: 225 Franklin Street, Suite 3100
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30B
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/348,548
;; FILING DATE: 01-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 06132/009001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-5070
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 127 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-348-548-4

Query Match 87.0%; Score 47; DB 3; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.41;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
Db 45 ASQDINNYLN 54

RESULT 39
PCT-US95-15716-4
; Sequence 4, Application PC/TUS9515716
; GENERAL INFORMATION:
; APPLICANT: Berdoz, Jose
; APPLICANT: Kirehenbuhl, Jean Pierre
; TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
; TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15716
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,548
; FILING DATE: 01-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06132/009001
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-5070
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 127 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US95-15716-4

Query Match 87.0%; Score 47; DB 5; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.41;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
Db 45 ASQDINNYLN 54

RESULT 40
US-08-425-763-1
; Sequence 1, Application US/08425763
; Patent No. 5641870
; GENERAL INFORMATION:
; APPLICANT: Rinderknecht, Ernst H.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY PURIFICATION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,763
; FILING DATE: 20-APR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 941
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-425-763-1

Query Match 87.0%; Score 47; DB 1; Length 214;
Best Local Similarity 90.0%; Pred. No. 0.74;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
Db 25 ASQDINNYLN 34

Mon Dec 20 08:54:48 2004

us-10-089-500-6.rat

Page 15

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Job time : 7.67416 secs

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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:20:33 ; Search time 21.2584 seconds
(without alignments)
185.159 Million cell updates/sec

Title: US-10-089-500-6
Perfect score: 54
Sequence: 1 SASODISNYLN 11

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Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
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3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	54	100.0	11	14	US-10-234-671-4
3	54	100.0	103	16	US-10-379-392-100
4	54	100.0	103	16	US-10-379-392-121
5	54	100.0	103	16	US-10-379-392-123
6	54	100.0	103	16	US-10-379-392-129
7	54	100.0	103	16	US-10-379-392-131
8	54	100.0	107	9	US-09-056-1608-13
9	54	100.0	107	9	US-09-056-1608-15
10	54	100.0	107	14	US-10-234-671-13
11	54	100.0	107	14	US-10-234-671-15
12	54	100.0	107	16	US-10-723-434-1
13	54	100.0	107	16	US-10-723-434-2

14	54	100.0	107	16	US-10-723-434-3
15	54	100.0	107	16	US-10-723-434-4
16	54	100.0	107	16	US-10-723-434-5
17	54	100.0	107	16	US-10-723-434-6
18	54	100.0	107	16	US-10-723-434-7
19	54	100.0	107	16	US-10-723-434-8
20	54	100.0	107	16	US-10-723-434-9
21	54	100.0	107	16	US-10-723-434-10
22	54	100.0	107	16	US-10-723-434-11
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24	54	100.0	107	16	US-10-723-434-13
25	54	100.0	107	16	US-10-723-434-14
26	54	100.0	108	9	US-09-056-1608-8
27	54	100.0	108	9	US-09-056-1608-10
28	54	100.0	108	9	US-09-056-1608-126
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30	54	100.0	108	13	US-10-153-159-4
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35	54	100.0	108	14	US-10-234-671-10
36	54	100.0	108	14	US-10-234-671-124
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38	54	100.0	108	15	US-10-443-134A-4
39	54	100.0	108	15	US-10-443-134A-16
40	54	100.0	108	15	US-10-443-134A-127
41	54	100.0	110	9	US-09-056-1608-103
42	54	100.0	110	9	US-09-056-1608-105
43	54	100.0	110	9	US-09-056-1608-107
44	54	100.0	110	9	US-09-056-1608-117
45	54	100.0	110	14	US-10-234-671-8

ALIGNMENTS

Sequence 3, Appl1
Sequence 4, Appl1
Sequence 5, Appl1
Sequence 6, Appl1
Sequence 7, Appl1
Sequence 8, Appl1
Sequence 9, Appl1
Sequence 10, Appl1
Sequence 11, Appl1
Sequence 12, Appl1
Sequence 13, Appl1
Sequence 14, Appl1
Sequence 16, Appl1
Sequence 126, App
Sequence 4, Appl1
Sequence 16, Appl1
Sequence 2, Appl1
Sequence 4, Appl1
Sequence 16, Appl1
Sequence 124, App
Sequence 2, Appl1
Sequence 4, Appl1
Sequence 16, Appl1
Sequence 127, App
Sequence 103, App
Sequence 107, App
Sequence 117, App
Sequence 8, Appl1

RESULT 1
US-09-056-1608-4
; Sequence 4, Application US/09056160B
; Patent No. US20020032315A1
GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
; NAME: Haesk, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1996
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-1608-4

Query Match 100.0%; Score 54; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
Db 1 SASQDISNYLN 11

RESULT 2
US-10-234-671-4
Sequence 4, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Welle, James A.
Preeta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-10-234-671-4

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-234-671-4

Query Match 100.0%; Score 54; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11

Db 1 SASQDISNYLN 11

RESULT 3
US-10-379-392-100
Sequence 100, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
Applicant: Desjardais, John Rudolf
Applicant: Marshall, Shannon Alicia
Applicant: Dahiyat, Basbil I
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 100
LENGTH: 103
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Humanized
US-10-379-392-100

Query Match 100.0%; Score 54; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
Db 24 SASQDISNYLN 34

RESULT 4
US-10-379-392-121
Sequence 121, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
Applicant: Desjardais, John Rudolf
Applicant: Marshall, Shannon Alicia
Applicant: Dahiyat, Basbil I
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 121
LENGTH: 103
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-379-392-121

Query Match 100.0%; Score 54; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11

Db 24 SASODISNTYLN 34

RESULT 5

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US-10-379-392-123
; Sequence 123, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjardais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basail I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-379-392-123
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Query Match 100.0%; Score 54; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SASODISNTYLN 11
Db 24 SASODISNTYLN 34
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RESULT 6

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US-10-379-392-129
; Sequence 129, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjardais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basail I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (36)..(36)
; OTHER INFORMATION: Xaa at position 36 can be Tyr, Phe, Met or Leu
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (43)..(43)
; OTHER INFORMATION: Xaa at position 43 can be Tyr, Phe, His, Asp, Thr, Ala, Asn or
; OTHER INFORMATION: Ser
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; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (87)..(87)
; OTHER INFORMATION: Xaa at position 87 can be Phe, Tyr or Met
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (89)..(89)
; OTHER INFORMATION: Xaa at position 89 can be Met or Gln
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (98)..(98)
; OTHER INFORMATION: Xaa at position 98 can be Phe or Tyr
US-10-379-392-129
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Query Match 100.0%; Score 54; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SASODISNTYLN 11
Db 24 SASODISNTYLN 34
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RESULT 7

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US-10-379-392-131
; Sequence 131, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjardais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basail I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 131
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-379-392-131
```

```
Query Match 100.0%; Score 54; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SASODISNTYLN 11
Db 24 SASODISNTYLN 34
```

RESULT 8

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US-09-056-160B-13
; Sequence 13, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
```

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haseak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-13

Query Match 100.0%; Score 54; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34

RESULT 9
US-09-056-160B-15
Sequence 15, Application US/09056160B
Patent No. US2002003215A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haseak, Janet E.

REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-15

Query Match 100.0%; Score 54; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34

RESULT 10
US-10-234-671-13
Sequence 13, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-10-234-671-13

Query Match 100.0%; Score 54; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTLN 11
 |||||
 Db 24 SASODISNTLN 34

RESULT 11

US-10-234-671-15
 ; Sequence 15, Application US/10234671
 ; Publication No. US20030190317A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baca, Manuel
 ; Wells, James A.
 ; Presta, Leonard G.
 ; Lowman, Henry B.
 ; Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
 NUMBER OF SEQUENCES: 131
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/234,671
 FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/056160
 FILING DATE: 06-APR-1998

APPLICATION NUMBER: 60/126446
 FILING DATE: 07-APR-1997

APPLICATION NUMBER: 60/054856
 FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Cui, Steven X.
 REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-8674
 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-10-234-671-15

Query Match 100.0%; Score 54; DB 14; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTLN 11
 |||||
 Db 24 SASODISNTLN 34

RESULT 12

US-10-723-434-1

; Sequence 1, Application US/10723434

; Publication No. US2004013357A1

; GENERAL INFORMATION:

; APPLICANT: Zhong, Pingyu

; APPLICANT: Luo, Peizhi

; APPLICANT: Wang, Kevin C.
 ; APPLICANT: Heien, Mark

; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR

; FILE REFERENCE: 26050-709.501

; CURRENT APPLICATION NUMBER: US/10/723,434

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 60/284,407

; PRIOR FILING DATE: 2001-04-17

; PRIOR APPLICATION NUMBER: US 10/125,687

; PRIOR FILING DATE: 2002-04-17

; PRIOR APPLICATION NUMBER: US 10/153,176

; PRIOR FILING DATE: 2002-05-20

; PRIOR APPLICATION NUMBER: US 10/443,134

; PRIOR FILING DATE: 2003-05-20

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: VL

US-10-723-434-1

Query Match 100.0%; Score 54; DB 16; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTLN 11
 |||||
 Db 24 SASODISNTLN 34

RESULT 13

US-10-723-434-2

; Sequence 2, Application US/10723434

; Publication No. US2004013357A1

; GENERAL INFORMATION:

; APPLICANT: Zhong, Pingyu

; APPLICANT: Luo, Peizhi

; APPLICANT: Wang, Kevin C.

; APPLICANT: Heien, Mark

; APPLICANT: Li, Yan

; FILE REFERENCE: 26050-709.501

; CURRENT APPLICATION NUMBER: US/10/723,434

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 60/284,407

; PRIOR FILING DATE: 2001-04-17

; PRIOR APPLICATION NUMBER: US 10/125,687

; PRIOR FILING DATE: 2002-04-17

; PRIOR APPLICATION NUMBER: US 10/153,176

; PRIOR FILING DATE: 2002-05-20

; PRIOR APPLICATION NUMBER: US 10/443,134

; PRIOR FILING DATE: 2003-05-20

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: VL

US-10-723-434-2

Query Match 100.0%; Score 54; DB 16; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
RESULT 14
US-10-723-434-3
; Sequence 3, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Heieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-3

Query Match      100.0%; Score 54; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASODISNYLN 11
Db      24 SASODISNYLN 34

RESULT 15
US-10-723-434-4
; Sequence 4, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Heieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
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```
US-10-723-434-4

Query Match      100.0%; Score 54; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASODISNYLN 11
Db      24 SASODISNYLN 34

RESULT 16
US-10-723-434-5
; Sequence 5, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Heieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-5

Query Match      100.0%; Score 54; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASODISNYLN 11
Db      24 SASODISNYLN 34

RESULT 17
US-10-723-434-6
; Sequence 6, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Heieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
```


;; PRIOR FILING DATE: 2003-05-20
;; NUMBER OF SEQ ID NOS: 156
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 6
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: VL
US-10-723-434-6

Query Match 100.0%; Score 54; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTYN 11
Db 24 SASODISNTYN 34

RESULT 18
US-10-723-434-7
; Sequence 7, Application US/10723434
; Publication No. US2004013357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Heieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-7

Query Match 100.0%; Score 54; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTYN 11
Db 24 SASODISNTYN 34

Query Match 100.0%; Score 54; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTYN 11
Db 24 SASODISNTYN 34

RESULT 19
US-10-723-434-8
; Sequence 8, Application US/10723434
; Publication No. US2004013357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Heieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501

;; CURRENT APPLICATION NUMBER: US/10/723,434
;; CURRENT FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: US 60/284,407
;; PRIOR FILING DATE: 2001-04-17
;; PRIOR APPLICATION NUMBER: US 10/125,687
;; PRIOR FILING DATE: 2002-04-17
;; PRIOR APPLICATION NUMBER: US 10/153,176
;; PRIOR FILING DATE: 2002-05-20
;; PRIOR APPLICATION NUMBER: US 10/443,134
;; PRIOR FILING DATE: 2003-05-20
;; NUMBER OF SEQ ID NOS: 156
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 8
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: VL
US-10-723-434-8

Query Match 100.0%; Score 54; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTYN 11
Db 24 SASODISNTYN 34

RESULT 20
US-10-723-434-9
; Sequence 9, Application US/10723434
; Publication No. US2004013357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Heieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-9

Query Match 100.0%; Score 54; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTYN 11
Db 24 SASODISNTYN 34

RESULT 21
US-10-723-434-10
; Sequence 10, Application US/10723434

```
Publication No. US20040133357A1
GENERAL INFORMATION:
APPLICANT: Zhong, Pingyu
APPLICANT: Luo, Peizhi
APPLICANT: Wang, Kevin C.
APPLICANT: Heieh, Mark
APPLICANT: Li, Yan
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
FILE REFERENCE: 26050-709.501
CURRENT APPLICATION NUMBER: US/10/723,434
PRIOR FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/443,134
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL
US-10-723-434-10
```

Query Match 100.0%; Score 54; DB 16; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 SASODISNYLN 11
    |||||
Db 24 SASODISNYLN 34
```

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RESULT 22
US-10-723-434-11
Sequence 11, Application US/10723434
Publication No. US20040133357A1
GENERAL INFORMATION:
APPLICANT: Zhong, Pingyu
APPLICANT: Luo, Peizhi
APPLICANT: Wang, Kevin C.
APPLICANT: Heieh, Mark
APPLICANT: Li, Yan
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
FILE REFERENCE: 26050-709.501
CURRENT APPLICATION NUMBER: US/10/723,434
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/443,134
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL
US-10-723-434-11
```

Query Match 100.0%; Score 54; DB 16; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 SASODISNYLN 11
    |||||
Db 24 SASODISNYLN 34
```

```
RESULT 23
US-10-723-434-12
Sequence 12, Application US/10723434
Publication No. US20040133357A1
GENERAL INFORMATION:
APPLICANT: Zhong, Pingyu
APPLICANT: Luo, Peizhi
APPLICANT: Wang, Kevin C.
APPLICANT: Heieh, Mark
APPLICANT: Li, Yan
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
FILE REFERENCE: 26050-709.501
CURRENT APPLICATION NUMBER: US/10/723,434
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/443,134
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL
US-10-723-434-12
```

Query Match 100.0%; Score 54; DB 16; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 SASODISNYLN 11
    |||||
Db 24 SASODISNYLN 34
```

```
RESULT 24
US-10-723-434-13
Sequence 13, Application US/10723434
Publication No. US20040133357A1
GENERAL INFORMATION:
APPLICANT: Zhong, Pingyu
APPLICANT: Luo, Peizhi
APPLICANT: Wang, Kevin C.
APPLICANT: Heieh, Mark
APPLICANT: Li, Yan
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
FILE REFERENCE: 26050-709.501
CURRENT APPLICATION NUMBER: US/10/723,434
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/443,134
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 107
```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL
US-10-723-434-13

Query Match 100.0%; Score 54; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTLN 11
DB 24 SASODISNTLN 34

RESULT 25

US-10-723-434-14
Sequence 14, Application US/10723434
Publication No. US2004013357A1
GENERAL INFORMATION:
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Peizhi
APPLICANT: Wang, Kevin C.
APPLICANT: Heien, Mark
APPLICANT: Li, Yan
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
FILE REFERENCE: 26050-709.501
CURRENT APPLICATION NUMBER: US/10/723,434
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/443,134
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 156
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL
US-10-723-434-14

Query Match 100.0%; Score 54; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTLN 11
DB 24 SASODISNTLN 34

RESULT 26

US-09-056-160B-8
Sequence 8, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B

FILING DATE: 06-Apr-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: P1093R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-056-160B-8

Query Match 100.0%; Score 54; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNTLN 11
DB 24 SASODISNTLN 34

RESULT 27

US-09-056-160B-10
Sequence 10, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-10

Query Match 100.0%; Score 54; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
|||
Db 24 SASQDISNYLN 34

RESULT 28
US-09-056-160B-126
Sequence 126, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:

APPLICANT: Baca, Mannel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896

INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-126

Query Match 100.0%; Score 54; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
|||
Db 24 SASQDISNYLN 34

RESULT 29

US-10-153-159-2
Sequence 2, Application US/10153159
Publication No. US20020177170A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Heieh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caili
TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
FILE REFERENCE: 26050-704
CURRENT APPLICATION NUMBER: US/10/153,159
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: VL of parental anti-VEGF antibody
US-10-153-159-2

Query Match 100.0%; Score 54; DB 13; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
|||
Db 24 SASQDISNYLN 34

RESULT 30
US-10-153-159-4
Sequence 4, Application US/10153159
Publication No. US20020177170A1
GENERAL INFORMATION:

APPLICANT: Luo, Peter
APPLICANT: Heieh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caili
TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
FILE REFERENCE: 26050-704
CURRENT APPLICATION NUMBER: US/10/153,159
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: VL of matured anti-VEGF antibody
US-10-153-159-4

Query Match 100.0%; Score 54; DB 13; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
|||
Db 24 SASQDISNYLN 34

RESULT 31
US-10-153-159-16
; Sequence 16, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Calli
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
; TITLE OF INVENTION: SILICO
; FILE REFERENCE: 26050-704
; CURRENT APPLICATION NUMBER: US/10/153,159
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 16
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of AM2-ccfv
US-10-153-159-16

Query Match 100.0%; Score 54; DB 13; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34

RESULT 32
US-10-153-176-2
; Sequence 2, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Calli
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of parental anti-VEGF antibody
US-10-153-176-2

Query Match 100.0%; Score 54; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34

DB 24 SASODISNYLN 34
RESULT 33
US-10-153-176-4
; Sequence 4, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Calli
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of matured anti-VEGF antibody
US-10-153-176-4

Query Match 100.0%; Score 54; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
DB 24 SASODISNYLN 34

RESULT 34
US-10-153-176-16
; Sequence 16, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Calli
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 16
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of AM2-ccfv
US-10-153-176-16

Query Match 100.0%; Score 54; DB 14; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASODISNTYLN 11
Db 24 SASODISNTYLN 34

RESULT 35

US-10-234-671-10
; Sequence 10, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-234-671-10
Query Match 100.0%; Score 54; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SASODISNTYLN 11
Db 24 SASODISNTYLN 34
RESULT 36
US-10-234-671-124
; Sequence 124, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel

Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160

FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-10-234-671-124
SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Query Match 100.0%; Score 54; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASODISNTYLN 11
Db 24 SASODISNTYLN 34

RESULT 37

US-10-443-134A-2
; Sequence 2, Application US/10443134A
; Publication No. US20040010376A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
; FILE REFERENCE: 26050-709
; CURRENT APPLICATION NUMBER: US/10/443,134A
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176

```
/ PRIOR FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: US 10/153,159
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of parental anti-VEGF antibody
US-10-443-134A-2
```

```
Query Match      100.0%; Score 54; DB 15; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SASODISNYLN 11
        |||||
Db      24 SASODISNYLN 34
```

```
RESULT 38
US-10-443-134A-4
/ Sequence 4, Application US/10443134A
/ Publication No. US20040010376A1
/ GENERAL INFORMATION:
/ APPLICANT: Luo, Peizhi
/ APPLICANT: Heieh, Mark
/ APPLICANT: Zhong, Pingyu
/ APPLICANT: Wang, Caili
/ APPLICANT: Cao, Yicheng
/ APPLICANT: Liu, Shengjiang
/ TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
/ FILE REFERENCE: 26050-709
/ CURRENT APPLICATION NUMBER: US/10/443,134A
/ PRIOR FILING DATE: 2003-05-20
/ PRIOR APPLICATION NUMBER: US 10/125,687
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: US 60/284,407
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: US 10/153,176
/ PRIOR FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: US 10/153,159
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of matured anti-VEGF antibody
US-10-443-134A-4
```

```
Query Match      100.0%; Score 54; DB 15; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SASODISNYLN 11
        |||||
Db      24 SASODISNYLN 34
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RESULT 39
US-10-443-134A-16
/ Sequence 16, Application US/10443134A
/ Publication No. US20040010376A1
/ GENERAL INFORMATION:
/ APPLICANT: Luo, Peizhi
/ APPLICANT: Heieh, Mark
/ APPLICANT: Zhong, Pingyu
/ APPLICANT: Wang, Caili
```

```
/ APPLICANT: Cao, Yicheng
/ APPLICANT: Liu, Shengjiang
/ TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
/ FILE REFERENCE: 26050-709
/ CURRENT APPLICATION NUMBER: US/10/443,134A
/ PRIOR FILING DATE: 2003-05-20
/ PRIOR APPLICATION NUMBER: US 10/125,687
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: US 60/284,407
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: US 10/153,176
/ PRIOR FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: US 10/153,159
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 16
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of AM2-ccFv
US-10-443-134A-16
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Query Match      100.0%; Score 54; DB 15; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SASODISNYLN 11
        |||||
Db      24 SASODISNYLN 34
```

```
RESULT 40
US-10-443-134A-127
/ Sequence 127, Application US/10443134A
/ Publication No. US20040010376A1
/ GENERAL INFORMATION:
/ APPLICANT: Luo, Peizhi
/ APPLICANT: Heieh, Mark
/ APPLICANT: Zhong, Pingyu
/ APPLICANT: Wang, Caili
/ APPLICANT: Cao, Yicheng
/ APPLICANT: Liu, Shengjiang
/ TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
/ FILE REFERENCE: 26050-709
/ CURRENT APPLICATION NUMBER: US/10/443,134A
/ PRIOR FILING DATE: 2003-05-20
/ PRIOR APPLICATION NUMBER: US 10/125,687
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: US 60/284,407
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: US 10/153,176
/ PRIOR FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: US 10/153,159
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 127
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of antibody X64, X65, D36, D40 and D42
US-10-443-134A-127
```

```
Query Match      100.0%; Score 54; DB 15; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SASODISNYLN 11
        |||||
Db      24 SASODISNYLN 34
```

Search completed: December 17, 2004, 18:38:00
Job time : 22.2584 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 18:11:22 ; Search time 4.32584 Seconds
(without alignments)
244.665 Million cell updates/sec

Title: US-10-089-500-6
Perfect score: 54
Sequence: 1 SASODISNYLN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	50	92.6	62 2 S42265	Ig kappa chain V r
2	50	92.6	87 2 I52592	Ig kappa chain V r
3	50	92.6	88 2 S34087	Ig kappa chain V r
4	50	92.6	88 2 S34088	Ig kappa chain V r
5	50	92.6	93 2 S38564	Ig kappa chain V r
6	50	92.6	95 2 PH0862	Ig kappa chain V r
7	50	92.6	107 2 S69901	Ig kappa chain V r
8	50	92.6	107 2 A28044	Ig kappa chain V r
9	50	92.6	107 2 D48677	Ig kappa chain V r
10	50	92.6	107 2 B28044	Ig kappa chain V r
11	50	92.6	107 2 B49026	Ig kappa chain V r
12	50	92.6	107 2 S69902	Ig kappa chain V r
13	50	92.6	108 1 KVM8AR	Ig kappa chain V r
14	50	92.6	108 2 PL0282	Ig kappa chain V r
15	50	92.6	108 2 C26405	Ig kappa chain V r
16	50	92.6	108 2 S38862	Ig kappa chain V r
17	50	92.6	108 2 S69902	Ig kappa chain V r
18	50	92.6	108 2 S69900	Ig kappa chain V r
19	50	92.6	108 2 S69903	Ig kappa chain V r
20	50	92.6	110 2 S44118	Ig kappa chain V r
21	50	92.6	115 2 A53276	Ig kappa chain V r
22	50	92.6	115 2 JL0080	Ig kappa chain V r
23	50	92.6	117 2 S42263	Ig kappa chain V r
24	50	92.6	117 2 S43528	Ig kappa chain V r
25	50	92.6	128 2 A26405	Ig kappa chain V r
26	50	92.6	129 2 S52789	Ig kappa chain V r
27	49	90.7	111 2 B37266	Ig kappa chain V r
28	49	90.7	111 2 G38740	Ig kappa chain V r
29	47	87.0	108 2 B26405	Ig kappa chain V r

30	47	87.0	111 2 A38740	Ig kappa chain V r
31	47	87.0	111 2 E38740	Ig kappa chain V r
32	47	87.0	111 2 C38740	Ig kappa chain V r
33	47	87.0	122 2 A29380	Ig kappa chain pre
34	47	87.0	126 2 A34904	Ig kappa chain pre
35	47	87.0	127 2 S52447	Ig kappa chain V r
36	46	85.2	108 2 S11124	Ig kappa chain V r
37	45	83.3	107 2 S32188	Ig kappa chain V r
38	45	83.3	108 1 K1H0AU	Ig kappa chain V r
39	45	83.3	109 2 PH0888	Ig kappa chain V r
40	45	83.3	111 2 I38740	Ig kappa chain V r
41	45	83.3	135 2 S24320	Ig kappa chain pre
42	44	81.5	105 2 PH0087	Ig kappa chain V r
43	44	81.5	108 2 S19674	Ig kappa chain V r
44	44	81.5	109 2 S31981	Ig kappa chain - h
45	44	81.5	127 2 S40367	Ig kappa chain V r

ALIGNMENTS

RESULT 1
S42265
Ig kappa chain V region (018) - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C/Accession: S42265
R/Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Quer
J. Immunol. 147, 4007-4013, 1991
A/Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf]
A/Reference number: S42263; WUID:92043792; PMID:1940382
A/Accession: S42265
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-62 <SCO>
A/Cross-references: EMBL:M64856
C/Genetics:
A/Intons: 19/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query Match 92.6%; Score 50; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ASQDISNYLN 11
DB 25 ASQDISNYLN 34

RESULT 2
152592
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C/Accession: I52592
R/Magner, S.D.; Martinielli, V.; Luzzatto, L.
Blood 83, 3647-3653, 1994
A/Title: Similar patterns of V kappa gene usage but different degrees of somatic mutator
A/Reference number: I52592; WUID:94264318; PMID:8204889
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-87 <RES>
A/Cross-references: GB:S71057; NID:9547053; PIDN:AAB30971.1; PID:9547054
C/Genetics:
A/Gene: I9KV
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/9-83/Domain: immunoglobulin homology <IMM>
Query Match 92.6%; Score 50; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASODISNYLN 11
 |||||
 18 ASODISNYLN 27

RESULT 3

S34087
 Ig kappa chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S34087
 R/Magner, S.D.; Luzzatto, L.
 Eur. J. Immunol. 23, 391-397, 1993
 A/Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
 A/Reference number: S34076; PMID:93170387; PMID:8436174
 A/Accession: S34087
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-88 <MAG>
 A/Cross-references: EMBL:X67171
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASODISNYLN 11
 |||||
 18 ASODISNYLN 27

RESULT 4

S34088
 Ig kappa chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S34088
 R/Magner, S.D.; Luzzatto, L.
 Eur. J. Immunol. 23, 391-397, 1993
 A/Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
 A/Reference number: S34076; PMID:93170387; PMID:8436174
 A/Accession: S34088
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-88 <MAG>
 A/Cross-references: EMBL:X67172
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASODISNYLN 11
 |||||
 18 ASODISNYLN 27

RESULT 5

S38564
 Ig kappa chain V region (ASMU1) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S38564
 R/Monestier, M.; Loeman, L.J.; Novick, K.E.; Aris, J.P.
 submitted to the EMBL Data Library, September 1993
 A/Description: Molecular analysis of mercury-induced anti-nuclear antibodies in H-2s M
 A/Reference number: S38559
 A/Accession: S38564

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-93 <MON>
 A/Cross-references: EMBL:X75105; NID:G414153; PIDN:CAA52996.1; PID:G414154
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASODISNYLN 11
 |||||
 25 ASODISNYLN 34

RESULT 6

PH0862
 Ig kappa chain V region (anti-DNA, III-3R) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
 C/Accession: PH0862
 R/Mahmmer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
 U. Exp. Med. 174, 1639-1652, 1991
 A/Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.
 A/Reference number: PH0862; PMID:92078875; PMID:1660528
 A/Accession: PH0862
 A/Molecule type: DNA
 A/Residues: 1-95 <MAN>
 A/Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F;1-23/Region: framework 1
 F;16-90/Domain: immunoglobulin homology <IMM>
 F;24-34/Region: complementarity-determining 1
 F;35-49/Region: framework 2
 F;50-56/Region: complementarity-determining 2
 F;57-88/Region: framework 3
 F;89-95/Region: complementarity-determining 3

Query Match 92.6%; Score 50; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASODISNYLN 11
 |||||
 25 ASODISNYLN 34

RESULT 7

S69901
 Ig kappa chain (clone KL2.21) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C/Accession: S69901
 R/Wysocki, L.J.; Creason, G.; Lehmann, K.R.; Cambier, J.C.
 Immunology 75, 116-121, 1992
 A/Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
 A/Reference number: S69900; PMID:92165291; PMID:1537587
 A/Accession: S69901
 A/Status: preliminary; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-107 <WYS>
 A/Cross-references: EMBL:X55042; NID:G511025; PIDN:CAA38882.1; PID:G511026
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASODISNYLN 11

Db 25 ASODISNYLN 34

RESULT 8

A28044

Ig kappa chain V region (22B5) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jan-2000

C/Accession: A28044

R/Week, K.; Sanz, I.; Rathbun, G.; Nisomoff, A.; Capra, J.D.

Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987

A/Title: Identity of the V-kappa-10-18-A gene segments of the A/J and BALB/c strains.

A/Reference number: A94179; PMID:87317629; PMID:3114744

A/Accession: A28044

A/Molecule type: mRNA

A/Residues: 1-107 <ME>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASODISNYLN 11
Db 25 ASODISNYLN 34

RESULT 9

D48677

Ig kappa chain V-J region (24) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000

C/Accession: D48677

R/Tasligon, J.; Bralt, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Haemann, C.

Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993

A/Title: Molecular characterization of monoclonal CRI-A-positive anti-arsenate antibodies

A/Reference number: A48677; PMID:94022404; PMID:8415731

A/Accession: D48677

A/Status: preliminary; not compared with conceptual translation

A/Residues: 1-107 <TAS>

A/Molecule type: mRNA

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASODISNYLN 11
Db 25 ASODISNYLN 34

RESULT 10

B28044

Ig kappa chain V region (GP1) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jan-2000

C/Accession: B28044

R/Week, K.; Sanz, I.; Rathbun, G.; Nisomoff, A.; Capra, J.D.

Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987

A/Title: Identity of the V-kappa-10-18-A gene segments of the A/J and BALB/c strains.

A/Reference number: A94179; PMID:87317629; PMID:3114744

A/Accession: B28044

A/Molecule type: mRNA

A/Residues: 1-107 <ME>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASODISNYLN 11
Db 25 ASODISNYLN 34

RESULT 11

B49026

Ig kappa chain V region, anti-idiotypic monoclonal antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C/Accession: B49026; PI0220

R/Koizumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.; Schwartz, R.S.

Eur. J. Immunol. 21, 2185-2193, 1991

A/Title: Molecular heterogeneity of auto-anti-idiotypic antibodies in MRL-1pr/1pr mice.

A/Reference number: A49026; PMID:91364791; PMID:1909645

A/Accession: B49026

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-107 <KOI>

A/Experimental source: MRL-1pr/1pr

A/Note: sequence extracted from NCBI backbone (NCBI:60876)

R/Puccetti, A.; Koizumi, T.; Migliorini, P.; Andre-Schwartz, J.; Barrett, K.J.; Schwartz, J.

Exp. Med. 171, 1919-1930, 1990

A/Title: An immunoglobulin light chain from a lupus-prone mouse induces autoantibodies in

A/Reference number: PI0220; PMID:90278348; PMID:1693654

A/Accession: PI0220

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-107 <PUC>

A/Experimental source: strain lupus-prone MRL-1pr/1pr mouse

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

F/24-34/Region: complementarity-determining 1

F/50-56/Region: complementarity-determining 2

F/89-97/Region: complementarity-determining 3

Query Match 92.6%; Score 50; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASODISNYLN 11
Db 25 ASODISNYLN 34

RESULT 12

S69906

Ig kappa chain (clone KL4A1) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S69906

R/Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambler, J.C.

Immunology 75, 116-121, 1992

A/Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin

A/Reference number: S69900; PMID:92165291; PMID:15337587

A/Accession: S69906

A/Status: preliminary; translation not shown

A/Molecule type: DNA

A/Residues: 1-107 <WYS>

A/Cross-references: EMBL:X55047; NID:G511035; PIDN:CAA3887.1; PID:G511036

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
|||||
DB 25 ASODISNYLN 34

RESULT 13

KWSAR

Ig kappa chain V regions (anti-arsenate hydridoma proteins) - mouse
C/Species: Mus musculus (house mouse)

C/Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
C/Accession: A01927

R.Siegelman, M.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981

A/Title: Complete amino acid sequence of light chain variable regions derived from five
A/Reference number: A01927; MUID:82150934; PMID:6801658

A/Accession: A01927
A/Molecule type: protein
A/Residues: 1-108 <SITE>

A/Cross-references: UNIPROT:P01644
A/Experimental source: strain A/J

A/Note: hp 93G7 differs in having 93-Met; HP 123B6 differs in having 7-Ser, 92-Tyr, and
Arg, 84-Ser, and 93-Ala

C/Comment: The sequence shown is HP R16.7.

C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862

R.Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993

A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S38862

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <PTS>

A/Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862

R.Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993

C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jan-2000
C/Accession: PL0282

R.Wysocki, L.J.; Gelfer, M.L.; Margolies, M.N.
J. Exp. Med. 172, 315-323, 1990

A/Title: Parallel evolution of antibody variable regions by somatic processes: Consequent
Y point mutation and selection rather than by gene conversion.
A/Reference number: PL0281; MUID:90293694; PMID:2358780
A/Accession: PL0282

A/Molecule type: mRNA
A/Residues: 1-108 <WYS>

A/Experimental source: A/J mice
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C/Accession: S69902

R.Wysocki, L.J.; Creason, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992

A/Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A/Reference number: S69900; MUID:92165291; PMID:1537587
A/Accession: S69902

A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <WYS>

A/Cross-references: EMBL:X55043; NID:g511027; PID:CA38883.1; PID:g511028
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C/Accession: C26405

RESULT 15

QY 2 ASODISNYLN 11
|||||
DB 25 ASODISNYLN 34

Ig kappa chain V region (3D10) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C/Accession: C26405

R.Smith, J.A.; Margolies, M.N.
Biochemistry 26, 604-612, 1987

A/Title: Complete amino acid sequences of the heavy and light chain variable regions from
A/Reference number: A90518; MUID:87157677; PMID:3103682
A/Accession: C26405

A/Molecule type: protein
A/Residues: 1-108 <SMI>

A/Experimental source: strain A/J
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862

R.Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993

A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S38862

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <PTS>

A/Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862

R.Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993

A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S38862

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <PTS>

A/Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862

R.Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993

A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S38862

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <PTS>

A/Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862

R.Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993

A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S38862

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <PTS>

A/Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862

R.Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993

A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S38862

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <PTS>

A/Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862

R.Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993

A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S38862

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <PTS>

A/Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862

R.Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993

A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S38862

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <PTS>

A/Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862

Db 25 ASODISNYLN 34

RESULT 18

S69900
Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C/Accession: S69900, S69907, S69908
R/Wysocki, L.J.; Creason, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A/Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A/Reference number: S69900; PMID:92165291; PMID:1537587
A/Accession: S69900
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <WYS>
A/Cross-references: EMBL:X55041; NID:G511023; PIDN:CAA38881.1; PID:G511024
A/Accession: S69907
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <WY2>
A/Cross-references: EMBL:X55048; NID:G511037; PIDN:CAA3888.1; PID:G511038
A/Accession: S69908
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <WY3>
A/Cross-references: EMBL:X55049; NID:G511039; PIDN:CAA38889.1; PID:G511040
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 19

S69903
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C/Accession: S69903, S69904, S69905
R/Wysocki, L.J.; Creason, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A/Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A/Reference number: S69900; PMID:92165291; PMID:1537587
A/Accession: S69903
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <WYS>
A/Cross-references: EMBL:X55044; NID:G511029; PIDN:CAA38884.1; PID:G511030
A/Accession: S69904
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <WY2>
A/Cross-references: EMBL:X55045; NID:G511031; PIDN:CAA38885.1; PID:G511032
A/Accession: S69905
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <WY3>
A/Cross-references: EMBL:X55046; NID:G511033; PIDN:CAA38886.1; PID:G511034
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASODISNYLN 11
Db 25 ASODISNYLN 34

RESULT 20

S4418
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C/Accession: S4418
R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A/Reference number: S44105
A/Accession: S4418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-110 <HAW>
A/Cross-references: EMBL:Z31395; NID:G472972; PIDN:CAA83270.1; PID:G940529
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASODISNYLN 11
Db 25 ASODISNYLN 34

RESULT 21

A53276
Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C/Accession: A53276
R/Kim, S.O.; Sanz, I.; Williams, C.; Capra, J.D.; Gottlieb, P.D.
Immunogenetics 34, 231-241, 1991
A/Title: Polymorphism in V kappa 10 genes encoding L chains of antibodies bearing the Ar
A/Reference number: A53276; PMID:92010099; PMID:1916951
A/Accession: A53276
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-115 <KIM>
A/Experimental source: AJ1 strain
A/Note: sequence extracted from NCBI backbone (NCBI:62777, NCBI:62780)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASODISNYLN 11
Db 45 ASODISNYLN 54

RESULT 22

JL0080
Ig kappa chain precursor V region (anti-phenylloxazolone, 16C10) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C/Accession: JL0080
R/Karinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A/Title: Combinatorial association of V genes: one VH gene codes for three non-cross-react
A/Reference number: JL0076; PMID:8906973; PMID:3211160
A/Accession: JL0080

A:Molecule type: mRNA
 A:Residues: 1-115 <RNA>
 A:Cross-references: GB:M2793; NID:g197161; PIDN:AAA38937.1; PID:g197162
 A>Note: the authors translated the codon AGG for residue 30 as Ser
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keyword: immunoglobulin
 F:1-6/Domain: signal sequence (fragment) #status predicted <SIG>
 F:7-115/Product: Ig light chain #status predicted <MAT>
 F:22-96/Domain: immunoglobulin homology <IMM>
 F:30-40/Region: complementarity-determining 1
 F:56-62/Region: complementarity-determining 2

Query Match 92.6%; Score 50; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
 |||||
 DB 31 ASODISNYLN 40

RESULT 23

S42263

Ig kappa chain V region (08) - human
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S42263
 R:Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
 J.; Immunol. 147, 4007-4013, 1991
 A>Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf
 A:Reference number: S42263; PMID:92043792; PMID:1940382
 A:Accession: S42263
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-117 <SCO>
 A:Cross-references: EMBL:M64855; NID:g185963; PIDN:AAA58925.1; PID:g185964
 C:Genetics:
 A:Intons: 19/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
 |||||
 DB 47 ASODISNYLN 56

RESULT 24

S43528

Ig kappa chain V region (018) - human
 C:Species: Homo sapiens (man)
 C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: S43528
 R:Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
 submitted to the EMBL Data Library, December 1991
 A:Reference number: S43528
 A:Accession: S43528
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-117 <SCO>
 A:Cross-references: EMBL:M64856
 C:Genetics:
 A:Intons: 19/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
 |||||
 DB 47 ASODISNYLN 56

RESULT 25

A26406

Ig kappa chain V region (Arb-A) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C:Accession: A26406
 R:Sanz, I.; Capra, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 84, 1085-1089, 1987
 A>Title: V-K and J-K gene segments of A/J Arb-A antibodies: somatic recombination generat
 A:Reference number: A26406; PMID:87147197; PMID:3103124
 A:Accession: A26406
 A:Molecule type: DNA
 A:Residues: 1-128 <SAN>
 A:Cross-references: UNIPROT:Q91WFB; GB:M15519
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 0.063;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
 |||||
 DB 45 ASODISNYLN 54

RESULT 26

S52789

Ig kappa chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: S52789
 R:Rocca, A.; Khamilichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,
 submitted to the EMBL Data Library, March 1995
 A>Description: light chain V region gene usage restriction and peculiarities in myeloma-
 A:Reference number: S52789
 A:Accession: S52789
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-129 <ROC>
 A:Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 129;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
 |||||
 DB 47 ASODISNYLN 56

RESULT 27

B37266

Ig kappa chain V region (2G8) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
 C:Accession: B37266
 R:Ruif-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
 J. Biol. Chem. 266, 6607-6613, 1991
 A>Title: Heavy and light chain variable region sequences and antibody properties of anti-
 A:Reference number: A38740; PMID:91177923; PMID:1706720
 A:Accession: B37266
 A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 49; DB 2; Length 111;
Best Local Similarity 90.0%; Pred. No. 0.083;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SASODISNYLN 11
|||||
DB 28 ASQDVSNYLN 37

RESULT 28

G38740
Ig kappa chain V region (Py69) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: G38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; PMID:91177923; PMID:1706720
A:Accession: G38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 49; DB 2; Length 111;
Best Local Similarity 90.9%; Pred. No. 0.083;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
|||||
DB 27 SASODIRNYLN 37

RESULT 29

B26405
Ig kappa chain V region (1F6) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26405
R:Smith, J.A.; Margolies, M.N.
Biochemistry 26, 604-612, 1987
A:Title: Complete amino acid sequences of the heavy and light chain variable regions fr
A:Reference number: A90518; PMID:87157677; PMID:3103682
A:Accession: B26405
A:Molecule type: protein
A:Residues: 1-108 <SMI>
A:Experimental source: strain A/J
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.19;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
|||||
DB 25 ASQDINNYLN 34

RESULT 30

A38740

Ig kappa chain V region (Py20) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: A38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; PMID:91177923; PMID:1706720
A:Accession: A38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

Query Match 87.0%; Score 47; DB 2; Length 111;
Best Local Similarity 90.9%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
|||||
DB 27 SASQGISNYLN 37

RESULT 31

E38740
Ig kappa chain V region (Py54) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: E38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; PMID:91177923; PMID:1706720
A:Accession: E38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 111;
Best Local Similarity 90.9%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
|||||
DB 27 SASQGISNYLN 37

RESULT 32

G38740
Ig kappa chain V region (Py2) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: G38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; PMID:91177923; PMID:1706720
A:Accession: G38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 111;
Best Local Similarity 90.9%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
|||||
DB 27 SASQGISNYLN 37

RESULT 33

A38740

Query Match 87.0%; Score 47; DB 2; Length 111;
Best Local Similarity 90.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
|||||
Db 27 SASQGISNYLN 37

RESULT 33

A39380

Ig kappa chain precursor V region (AC-1001) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000

C/Accession: A29380

R/Chem, H.T./Kabat, E.A./Lundblad, A./Ratcliffe, R.M.

J. Biol. Chem. 262, 13579-13583, 1987

A/Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable

A/Reference number: A92612; MWID:88007582; PMID:3115961

A/Accession: A29380

A/Molecule type: mRNA

A/Residues: 1-122 <CH>

A/Cross-references: GB:M17160; GB:J02815; NID:g196695; PIDN:AAA38824.1; PID:g196696

A/Note: the authors translated the codon TTC for residue 1 as Leu

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/30-104/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 122;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
|||||
Db 39 ASQDINNYLN 48

RESULT 34

A34904

Ig kappa chain precursor V region (5-27) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004

C/Accession: A34904

R/Bedyk, W.D./Herron, J.N./Edmundson, A.B./Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990

A/Title: Active site structure and antigen binding properties of idiotypically cross-react

A/Reference number: A34903; MWID:90094387; PMID:2104617

A/Accession: A34904

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-126 <BED>

A/Cross-references: UNIPROT:Q91WF8

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/35-109/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 126;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
|||||
Db 44 ASQDINNYLN 53

RESULT 35

S52447

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C/Accession: S52447

R/Berdoz, J./Kraehenbuhl, J.P.

submitted to the EMBL Data Library, November 1994

A/Description: Specific amplification by the polymerase chain reaction of rearranged genc

A/Reference number: S52445

A/Accession: S52447

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-127 <BER>

A/Cross-references: EMBL:X82688; NID:g673443; PIDN:CAA56009.1; PID:g673444

C/Genetics:

A/Introns: 17/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
|||||
Db 45 ASQDINNYLN 54

RESULT 36

S11124

Ig kappa chain V region (clone N05-89.4) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000

C/Accession: S11124

R/Karttinen, M./Griffiths, G.M./Marham, A.F./Milestein, C.

Nature 304, 320-324, 1983

A/Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone

A/Reference number: S07331; MWID:83271467; PMID:6877353

A/Accession: S11124

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-108 <KAA>

A/Note: 87-Pne was also found

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 46; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SODISNYLN 11
|||||
Db 26 SODISNYLN 34

RESULT 37

S32188

Ig kappa chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C/Accession: S32188

R/Izui, S.

submitted to the EMBL Data Library, February 1993

A/Reference number: S32185

A/Accession: S32188

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-107 <IZU>

A/Cross-references: EMBL:X70090; NID:g288253; PIDN:CAA49695.1; PID:g288254

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.43;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
|||||

Db 25 ASODISNYLN 34

RESULT 38

KIHUAV

Ig kappa chain V-I region (Au) - human

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004

C/Accession: A91653; A01862; S02573

R/Schleichl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972

A/Title: Die Primarstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ. Sub

A/Reference number: A91653; PMID:72189444; PMID:5028201

A/Accession: A91653

A/Molecule type: protein

A/Residues: 1-108 <SCH>

A/Cross-references: UNIPROT:P01594

A/Note: the C region of this chain has the Inv (3) marker

R/Fehlhammer, H.; Schliefer, M.; Bp, O.; Colman, P.M.; Lattman, E.B.; Schwager, P.; Stei

Biophys. Struct. Mech. 1, 139-146, 1975

A/Title: The structure determination of the variable portion of the Bence-Jones protein

A/Reference number: A90729; PMID:77022433; PMID:1234024

A/Contents: annotation; X-ray crystallography

A/Note: the structure of the V region was determined by molecular replacement methods us

R/Steiner, V.; Chang, J.Y.

FEBS Lett. 222, 6-10, 1987

A/Title: Chemical modification of the carboxyl groups of protein substrates enhances the

A/Reference number: S02572; PMID:88005152; PMID:3115831

A/Contents: annotation

C/Comment: This is a Bence Jones protein.

C/Genetics:

A/Gene: GDB:IGKV1

A/Cross-references: GDB:136264

A/Map position: 2p12-2p12

C/Complex: an immunoglobulin heterotetramer subunit consists of two identical light (ka

chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

F:23-88/Disulfide bonds: Metacis predicted

Query Match 83.3%; Score 45; DB 1; Length 108;

Best Local Similarity 90.0%; Pred. No. 0.44;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11

Db 25 ASODISDYN 34

RESULT 39

PH0888

Ig kappa chain V region (anti-CD3) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000

C/Accession: PH0888

R/Shalaby, M.R.; Shepard, H.M.; Prestra, L.; Rodriguez, M.L.; Beverley, P.C.L.; Feldmann,

J. Exp. Med. 175, 217-225, 1992

A/Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocy

A/Reference number: PH0885; PMID:92113462; PMID:1346155

A/Accession: PH0888

A/Molecule type: mRNA

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 109;

Best Local Similarity 90.0%; Pred. No. 0.44;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11

Db 25 ASODIRNYLN 34

RESULT 40

I38740

Ig kappa chain V region (Py42) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000

C/Accession: I38740

R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A/Title: Heavy and light chain variable region sequences and antibody properties of anti-

A/Reference number: A38740; PMID:91177923; PMID:1706720

A/Accession: I38740

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A/Molecule type: mRNA

A/Residues: 1-111 <RUF>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 111;

Best Local Similarity 90.0%; Pred. No. 0.45;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11

Db 28 ASODASNYLN 37

Search completed: December 17, 2004, 18:30:15
Job time : 5.32584 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw-model

Run on: December 17, 2004, 18:29:23 ; Search time 32.8764 Seconds
(without alignments)
192.513 Million cell updates/sec

Title: US-10-089-500-6
Perfect score: 54
Sequence: 1 SASODISNYLN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	54	100.0	108 1 KVSU_MOUSE	P04946 mus musculu
2	50	92.6	50 2 Q6LHV5	Q6LHV5 homo sapien
3	50	92.6	50 2 CAE82012	CAE82012 mus sapi
4	50	92.6	108 1 KVSU_MOUSE	P01644 mus musculu
5	50	92.6	108 1 KVSU_MOUSE	P01645 mus musculu
6	50	92.6	108 1 KVSU_MOUSE	P01646 mus musculu
7	50	92.6	111 2 AAR10992	AAR10992 mus muscu
8	50	92.6	234 2 Q91WF8	Q91WF8 mus musculu
9	47	87.0	108 1 KVSU_MOUSE	P01647 mus musculu
10	47	87.0	108 1 KVSU_MOUSE	P01648 mus musculu
11	47	87.0	234 2 Q8R062	Q8R062 mus musculu
12	46	85.2	104 2 AAR11000	AAR11000 mus muscu
13	45	83.3	104 1 AAR11043	AAR11043 mus muscu
14	45	83.3	108 1 KVLB_HUMAN	P01594 homo sapien
15	44	81.5	107 2 Q9ULB1	Q9ULB1 homo sapien
16	44	81.5	108 1 KVLV_HUMAN	P04331 homo sapien
17	44	81.5	129 1 KVLW_HUMAN	P04431 homo sapien
18	44	81.5	236 2 Q7Z3Y4	Q7Z3Y4 homo sapien
19	42	77.8	103 2 AAR11052	AAR11052 mus muscu
20	42	77.8	108 1 KVLH_HUMAN	P01593 homo sapien
21	42	77.8	116 2 Q96PF6	Q96PF6 homo sapien
22	42	77.8	236 2 Q6GKX0	Q6GKX0 homo sapien
23	41	75.9	108 1 KVSU_MOUSE	P01643 mus musculu
24	41	75.9	859 2 Q7PDL4	Q7PDL4 plasmodium
25	40	74.1	233 2 Q91WS9	Q91WS9 mus musculu
26	40	74.1	583 2 Q6LZM4	Q6LZM4 methanococc
27	40	74.1	583 2 CAF30065	CAF30065 methanoco
28	40	74.1	956 2 O8ILX3	O8ILX3 plasmodium
29	40	74.1	1116 2 Q7RDE1	Q7RDE1 plasmodium
30	40	74.1	7500 2 Q7KTP3	Q7KTP3 drosophila
31	40	74.1	7500 2 AAS64640	AAS64640 drosophila

32	40	74.1	7735 2 Q9VMT8	Q9VMT8 drosophila
33	39	72.2	107 2 Q96SA9	Q96SA9 homo sapien
34	39	72.2	108 2 Q9UL177	Q9UL177 homo sapien
35	39	72.2	117 1 KVSU_MOUSE	P01641 mus musculu
36	39	72.2	225 2 Q9X556	Q9X556 enterococcu
37	39	72.2	461 2 Q838Y1	Q838Y1 enterococcu
38	39	72.2	506 2 Q9H192	Q9H192 thermoplasma
39	39	72.2	1093 2 Q8EV69	Q8EV69 mycoplasma
40	39	72.2	1665 2 Q7PDL3	Q7PDL3 plasmodium
41	38	70.4	67 2 Q8YXN0	Q8YXN0 anabaena sp
42	38	70.4	108 1 KVLV_HUMAN	P04331 homo sapien
43	38	70.4	433 2 Q7V117	Q7V117 prochloroco
44	38	70.4	443 2 Q7N5S4	Q7N5S4 photorhabdu
45	38	70.4	581 2 Q6N1A8	Q6N1A8 corynebacte

ALIGNMENTS

RESULT 1
KVSU_MOUSE
ID KVSU_MOUSE STANDARD; PRT; 108 AA.

AC P04946;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE IG kappa chain V-V region NQ5-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenylloxazolone and its early diversification".
RL Nature 304:320-324(1983).

CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.

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CC EMBL; K00745; AAA38690.1; -.
DR HSSP; P01594; JUV5.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Igy_1.
DR SMART; SM00406; Igy_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DD CRC64;

Query Match 100.0%; Score 54; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
|||||

Db 24 SASQDISNYLN 34

RESULT 2

ID O6LBVS PRELIMINARY; PRT; 50 AA.

AC O6LBVS, 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

RT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE DNA rearranged by a t(2;8) translocation leading to Burkitt's lymphoma in the cell line JI (clone JIP) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8725967; PubMed=3110741;

RA Klobbeck H.G., Combrato G., Zachau H.G.,

RT "N segment insertion and region directed somatic hypermutation in a kappa gene of a t (2;8) chromosomal translocation.",

RL Nucleic Acids Res. 15:4877-4888(1987).

DR EMBL; X05929; CA82012.1; -.

DR InterPro; IPR007110; Ig-like.

FT NON_TER 1

FT SEQUENCE 50 AA; 5486 MW; 3A74178720E0DA21 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 50; Best Local Similarity 100.0%; Pred. No. 0.086; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11
28 ASQDISNYLN 37

RESULT 3

ID CA82012 PRELIMINARY; PRT; 50 AA.

AC CA82012;

DT 02-MAR-2004 (TREMBlrel. 27, Created)

RT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)

DE Human DNA rearranged by a t(2;8) translocation leading to Burkitt's lymphoma in the cell line JI (clone JIP) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE OF 35-50 FROM N.A.

RX MEDLINE=8725967; PubMed=3110741;

RA Klobbeck H.G., Combrato G., Zachau H.G.,

RT "N segment insertion and region directed somatic hypermutation in a kappa gene of a t (2;8) chromosomal translocation.",

RL Nucleic Acids Res. 15:4877-4888(1987).

DR EMBL; X05929; CA82012.1; -.

DR Chromosomal translocation; Oncogene.

FT NON_TER 1

FT SEQUENCE 50 AA; 5486 MW; 3A74178720E0DA21 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 50; Best Local Similarity 100.0%; Pred. No. 0.086; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11
28 ASQDISNYLN 37

RESULT 4

ID KV5K_MOUSE STANDARD; PRT; 108 AA.

AC P01644;

DT 21-JUL-1986 (Rel. 01, Created)

RT 21-JUL-1986 (Rel. 01, Last sequence update)

DE Ig kappa chain V-V region HP R16.7.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE.

RC STRAIN=A/J;

RX MEDLINE=82150934; PubMed=6801658;

RA Siegelman M., Capra J.D.;

RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idio type.",

RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).

DR PIR; A01927; KVM5AR.

DR HSSP; P01594; 1JVS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 1.

KM Direct protein sequencing; Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.

FT DOMAIN 24 34 Complementarity-determining-1.

FT DOMAIN 35 49 Framework-2.

FT DOMAIN 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.

FT DOMAIN 89 97 Complementarity-determining-3.

FT DOMAIN 98 108 Framework-4.

FT DISULFID 23 88 By similarity.

FT NON_TER 108

SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFP597 CRC64;

Query Match 92.6%; Score 50; DB 1; Length 108; Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11
25 ASQDISNYLN 34

RESULT 5

ID KV5L_MOUSE STANDARD; PRT; 108 AA.

AC P01645;

DT 21-JUL-1986 (Rel. 01, Created)

RT 21-JUL-1986 (Rel. 01, Last sequence update)

DE Ig kappa chain V-V region HP 93G7.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE.

RC STRAIN=A/J;

RX MEDLINE=82150934; PubMed=6801658;

RA Siegelman M., Capra J.D.;

RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idio type.",

RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).

CC -1- MISCELLANEOUS: Anti-arsenate hydridoma protein.

DR HSSP; P01607; IREI.

```

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 2 34
FT DOMAIN 3 49
FT DOMAIN 4 56
FT DOMAIN 5 78
FT DOMAIN 6 88
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EF58E CRC64;

Query Match
Best Local Similarity 92.6%; Score 50; DB 1; Length 108;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 2 ASODISNYLN 11
DB 25 ASODISNYLN 34

```

```

RESULT 6
KVSM_MOUSE STANDARD; PRT; 108 AA.
ID KVSM_MOUSE
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype".
RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hydridoma protein.
DR HSSP; P01594; IJVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 2 34
FT DOMAIN 3 49
FT DOMAIN 4 56
FT DOMAIN 5 78
FT DOMAIN 6 88
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08BBA09A CRC64;

```

```

Query Match
Best Local Similarity 92.6%; Score 50; DB 1; Length 108;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 ASODISNYLN 11
DB 25 ASODISNYLN 34

```

```

RESULT 7
AA10992 PRELIMINARY; PRT; 111 AA.
ID AA10992
AC AA10992;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.SleJ; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.SleJ mice."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436832; AA10992.1; -.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12120 MW; 879A9DB5880C59D CRC64;

```

```

Query Match
Best Local Similarity 92.6%; Score 50; DB 2; Length 111;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 22 ASODISNYLN 31

RESULT 8
Q91WF8 PRELIMINARY; PRT; 234 AA.
ID Q91WF8
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=2338257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Millaby S.J.,
RA Raha S.S., McMan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McMan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schenck A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;

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RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR PIR; A26406; A26406.
DR PIR; A34904; A34904.
DR PDB; 1JFQ; X-ray; l=21-234.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF07654; Cl-sec; 1.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KM Hypothetical protein
SQ SEQUENCE 234 AA; 25929 MW; B0DOB0E6E87812D2 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 45 ASQDISNYLN 54

RESULT 9

KVSN_MOUSE STANDARD; PRT; 108 AA.
ID KVSN_MOUSE
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."
RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEPF2 CRC64;

Query Match 87.0%; Score 47; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.71;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 25 ASQDISNYLN 34

RESULT 10

KVSO_MOUSE STANDARD; PRT; 108 AA.
ID KVSO_MOUSE
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."
RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; IUV5.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 87.0%; Score 47; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.71;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 25 ASQDISNYLN 34

RESULT 11

Q8R062 PRELIMINARY; PRT; 234 AA.
ID Q8R062;
AC Q8R062;
DT 01-JUN-2002 (TREMELREL. 21, Created)
DT 01-JUN-2002 (TREMELREL. 21, Last sequence update)
DT 01-MAR-2004 (TREMELREL. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rabe S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Boek S.A., Mesman P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Huliyil S.W.,
 RA Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC027418; AAH27418.1; -.
 DR HSSP; P01594; IUV5.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-sec; 1.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 2.
 DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein
 SQ SEQUENCE 234 AA; 25858 MW; 4EB08C81426AEAB1 CRC64;

Query Match 87.0%; Score 47; DB 2; Length 234;
 Best Local Similarity 90.9%; Pred. No. 1.6;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
 DB 44 SASODISNYLN 54
 RESULT 12
 AAR11000 PRELIMINARY; PRT; 104 AA.
 AC AAR11000;
 ID AAR11000 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE ANA Immunoglobulin kappa light chain (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S1e1; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.S1e1 mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436840; AAR11000.1; -.
 FT NON_TER 1
 FT NON_TER 104
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11250 MW; 014C270D5B104DC6 CRC64;

Query Match 85.2%; Score 46; DB 2; Length 104;
 Best Local Similarity 90.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ASODISNYLN 11

DB 15 ACODISNYLN 24
 RESULT 13
 AAR11043 PRELIMINARY; PRT; 104 AA.
 AC AAR11043;
 ID AAR11043 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE ANA Immunoglobulin kappa light chain (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S1e1; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.S1e1 mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436883; AAR11043.1; -.
 FT NON_TER 1
 FT NON_TER 104
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11473 MW; 58B393C037D426A7 CRC64;

Query Match 83.3%; Score 45; DB 2; Length 104;
 Best Local Similarity 90.0%; Pred. No. 1.6;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ASODISNYLN 11
 DB 22 ASODISNYLN 31

RESULT 14
 KYIB HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-I region AU.
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hlischmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlhammer H., Schiffer M., Epp O., Colman P.M., Iatman E.E.,
 RA Schwaiger P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the Bence-
 RT Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -I- MISCELLANEOUS; The structure of the V region was determined by
 CC molecular replacement methods using the known structure of the V
 CC region of the kappa chain R1.
 CC -I- MISCELLANEOUS; The C region of this chain has the INV (3) marker.
 CC -I- MISCELLANEOUS; This is a Bence-Jones protein.
 DR PIR; A91653; KIHUAV.
 DR PDB; 1UV5; X-ray; A=1-107.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.

DR	GO; GO:006955; P:Immune response; NAS.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KM	3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
KM	DOMAIN 1 23 Framework-1.
FT	DOMAIN 24 34 Complementarity-determining-1.
FT	DOMAIN 35 49 Framework-2.
FT	DOMAIN 50 56 Complementarity-determining-2.
FT	DOMAIN 57 88 Framework-3.
FT	DOMAIN 89 97 Complementarity-determining-3.
FT	DOMAIN 98 107 Framework-4.
FT	DISULFID 23 88 By similarity.
FT	STRAND 4 5
FT	STRAND 10 13
FT	TURN 15 16
FT	STRAND 19 25
FT	TURN 30 31
FT	STRAND 33 38
FT	TURN 40 41
FT	STRAND 44 49
FT	TURN 50 52
FT	STRAND 53 54
FT	TURN 56 57
FT	TURN 60 61
FT	STRAND 62 67
FT	TURN 68 69
FT	STRAND 70 75
FT	HELIK 80 82
FT	STRAND 85 90
FT	STRAND 97 98
FT	STRAND 102 106
FT	NON TER 108 108
SO	SEQUENCE 108 AA; 11939 MW; E801187BE6F6FB9 CRC64;
Qy	2 ASODISNTYN 11 Query Match 83.3%; Score 45; DB 1; Length 108; Best Local Similarity 90.0%; Pred. No. 1.7; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db	25 ASODISDTYN 34
RESULT 15	
09UL81	PRELIMINARY; PRT; 107 AA.
ID 09UL81	
AC 09UL81	
DT 01-MAY-2000 (TREMBLrel. 13, Created)	
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).	
DE Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX NCBI_TaxID=9606;	
OX NCBI_TaxID=9606;	
RN	SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;	
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;	
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";	
RT Clin. Immunol. Immunopathol. 87:184-192(1998).	
RL EMBL; AF035033; AAD56269.1; -.	
DR HSSP; P01607; 1BMW.	
DR InterPro; IPR007110; IG-like.	
DR InterPro; IPR003596; IG_v.	
DR Pfam; PF00047; Ig; 1.	

[illegible]


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FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 98 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match
Best Local Similarity 81.5%; Score 44; DB 1; Length 108;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
    |||||:|:|
    |||||:|:|
Db 25 ASODITNYVN 34

RESULT 17
KV1W_HUMAN STANDARD; PRT; 129 AA.
ID P04431;
AC 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region Walker precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combario G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X00965; CAA35477.1; ALT_TERM.
DR PIR, A01883; K1H0MK.
DR HSSP, P01607; 1BWM.
DR GO, GO:0005576; C:extracellular; NAS.
DR GO, GO:0003823; F:antigen binding; NAS.
DR GO, GO:0006955; P:immune response; NAS.
DR InterPro, IPR007110; IG-like.
DR InterPro, IPR003596; IG_V.
DR Pfam, PF00047; IG_1.
DR SMART, SM00406; IGV_1.
DR PROSITE, PS50835; IG LIKE_1.
KW Immunoglobulin V region, Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
    Ig kappa chain V-I region Walker.
    Framework-1.
    Complementarity-determining-1.
    Framework-2.
    Complementarity-determining-2.
    Framework-3.
    Complementarity-determining-3.
    Framework-4.
    Complementarity-determining-4.
    By similarity.
  
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FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFC2F9 CRC64;

Query Match
Best Local Similarity 81.5%; Score 44; DB 1; Length 129;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
    |||||:|:|
    |||||:|:|
Db 47 ASODISNYLN 56

RESULT 18
Q723Y4 PRELIMINARY; PRT; 236 AA.
ID Q723Y4;
AC Q723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Ketterman M., Madan A., Rodriguez Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman A., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smallus D.E., Scherch A., Schen J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC005332; AAH05332.1; -.
DR InterPro, IPR007110; IG-like.
DR InterPro, IPR003597; IG_C1.
DR InterPro, IPR003006; IG_MHC.
DR InterPro, IPR003596; IG_V.
DR Pfam, PF07654; C1-sect_1.
DR Pfam, PF00047; IG_1.
DR SMART, SM00406; IGV_1.
DR PROSITE, PS50835; IG LIKE_2.
DR PROSITE, PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match
Best Local Similarity 81.5%; Score 44; DB 2; Length 236;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 10
    |||||:|:|
    |||||:|:|
Db 47 ASODISNYLN 55
  
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RESULT 19
AA11052
ID AA11052 PRELIMINARY; PRT; 103 AA.
AC AA11052;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436892; AA11052.1; -.
FT NON_TER 1 1
SQ SEQUENCE 103 AA; 11332 MW; B103B7D98711B901 CRC64;

Query Match
Best Local Similarity 90.0%; Score 42; DB 2; Length 103;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 22 ASODISNYLN 31

RESULT 20
KV1A_HUMAN
ID KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges."
RL J. Biol. Chem. 244:3550-3560(1969).
CC -|- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-|- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01861; KIHUG.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR SMART; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
KL Kluener R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
FT DOMAIN 89 97

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FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match
Best Local Similarity 77.8%; Score 42; DB 1; Length 108;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 25 ASODISNYLN 34

RESULT 21
O96PF6
ID O96PF6 PRELIMINARY; PRT; 116 AA.
AC O96PF6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
GN Name=SDNK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
burden."
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
DR HSSP; P80362; 1WTU.
DR InterPro; IPR007110; Ig_V.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR SMART; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match
Best Local Similarity 77.8%; Score 42; DB 2; Length 116;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 25 ASODISNYLN 34

RESULT 22
O6GKX0
ID O6GKX0 PRELIMINARY; PRT; 236 AA.
AC O6GKX0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
KL Kluener R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
FT DOMAIN 57 88

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uediri T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE= spleen;
RA Struhsberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH7375.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-secl; 1.
DR Pfam; PF00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN; 1.
DR Hypothetical protein.
KW SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;
SQ

Query Match 77.8%; Score 42; DB 2; Length 236;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SASQDISNYLN 11
DB 47 ASQININYNLN 56

RESULT 23
KV5J MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-V region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
OX [1]
RN SEQUENCE.
RP MEDLINE=76091934; PubMed=812696;
RA Schiff C., Fougereau M.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC PIR; A01926; KVM573.
DR HSSP; P01594; 1YV5.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;
Query Match 75.9%; Score 41; DB 1; Length 108;
Best Local Similarity 72.7%; Pred. No. 9.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
DB 24 SASQDISNYLB 34

RESULT 24
Q7PDL4 PRELIMINARY; PRT; 859 AA.
ID Q7PDL4
AC Q7PDL4;
DT 01-MAR-2004 (TRENDEL. 26, Created)
DT 01-MAR-2004 (TRENDEL. 26, Last sequence update)
DE Erythrocyte membrane protein PREMP3.
GN Name=PY06116;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=1236865;
RA Carlton J.M., Anguillo S.V., Suh B.B., Koo J.T.W., Pereira M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut U.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalton S.J., van Aken S.E., Riedmiller S.B., Feldlyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabdi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.B., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Garucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002034; EAA18272.1; -.
DR InterPro; IPR002377; G_PROTEIN_RECIP_F1.1; UNKNOWN; 1.
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1.1; UNKNOWN; 1.
SQ SEQUENCE 859 AA; 96311 MW; 1C35C377A8DB8064 CRC64;
Query Match 75.9%; Score 41; DB 2; Length 859;
Best Local Similarity 63.6%; Pred. No. 88;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
DB 161 SAPSDVSNYNLN 171

RESULT 25
Q91WS9 PRELIMINARY; PRT; 233 AA.
ID Q91WS9
AC Q91WS9;

DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Stauber R.L., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein W., Udell T.B., Toshiyuki S., Carrinci P., Prange C.,
 RA Rana S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., Lequan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Kozlyanski M.I., Skalska U., Smatov D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Straubeberg R.;
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC013496; AAH13496.1; --
 DR PIR; A38740; A38740.
 DR PIR; C38740; C38740.
 DR PIR; E38740; E38740.
 DR PIR; G38740; G38740.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KM Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;
 QY 1 SASQDISNYIN 11
 Db 43 SSGSQGIANYIN 53
 RESULT 26
 Q6L2M4 PRELIMINARY; PRT; 583 AA.
 AC Q6L2M4;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE Formylmethanofuran dehydrogenase, subunit A (EC 1.2.99.5).
 DN Name=fmdA; OrderedLocustNames=WMP0509;

OC	Methanococcus maripaludis.
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC	Methanococcaceae; Methanococcus.
OC	NCBI_TaxID=39152;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	STRAIN=S2 / LL;
RA	Hendrickson E.L., Kaul R., Zhou Y., Boyee D., Chapman P., Chung J.,
RA	Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA	Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA	Moore B., Porat I., Overbeek R., Palmeri A., Rouse G.,
RA	Saenphitachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
RA	Leigh J.A.;
RT	"Complete genome sequence of the mesophilic hydrogenotrophic
RT	methanogen Methanococcus maripaludis.";
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL: BX957220, CAF30065.1; -
DR	GO: GO:0018493; F:formylmethanofuran dehydrogenase activity; IEA.
DR	GO: GO:0016491; F:oxidoreductase activity; IEA.
DR	InterPro: IPR011059; Meta10_hydro1ae.
KW	Complete proteome; Oxidoreductase.
SO	SEQUENCE 583 AA; 64594 MW; 76CF31FF5DA0263 CRC64;
QY	1 SASODISNYLN 11
DB	305 SKAEDISNYVN 315
RESULT 27	
CAF30065	PRELIMINARY; PRT; 583 AA.
ID	CAF30065
AC	CAF30065;
DT	03-MAR-2004 (TREMBlrel. 27, Created)
DT	03-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT	04-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE	Formylmethanofuran dehydrogenase, subunit A (BC 1.2.99.5).
GN	FMDA GN MWP0509.
OS	Methanococcus maripaludis.
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC	Methanococcaceae; Methanococcus.
OX	NCBI_TaxID=39152;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	STRAIN=S2 / LL;
RA	Hendrickson E.L., Kaul R., Zhou Y., Boyee D., Chapman P., Chung J.,
RA	Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA	Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA	Moore B., Porat I., Overbeek R., Palmeri A., Rouse G.,
RA	Saenphitachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
RA	Leigh J.A.;
RT	"Complete genome sequence of the mesophilic hydrogenotrophic
RT	methanogen Methanococcus maripaludis.";
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL: BX957220, CAF30065.1; -
DR	GO: GO:0018493; F:formylmethanofuran dehydrogenase activity; IEA.
DR	GO: GO:0016491; F:oxidoreductase activity; IEA.
DR	InterPro: IPR011059; Meta10_hydro1ae.
KW	Complete proteome; Oxidoreductase.
SO	SEQUENCE 583 AA; 64594 MW; 76CF31FF5DA0263 CRC64;
QY	1 SASODISNYLN 11
DB	305 SKAEDISNYVN 315
RESULT 28	
CAF30065	PRELIMINARY; PRT; 956 AA.
ID	CAF30065
AC	CAF30065;
DT	03-MAR-2004 (TREMBlrel. 27, Created)
DT	03-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT	04-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE	Formylmethanofuran dehydrogenase, subunit A (BC 1.2.99.5).
GN	FMDA GN MWP0509.
OS	Methanococcus maripaludis.
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC	Methanococcaceae; Methanococcus.
OX	NCBI_TaxID=39152;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	STRAIN=S2 / LL;
RA	Hendrickson E.L., Kaul R., Zhou Y., Boyee D., Chapman P., Chung J.,
RA	Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA	Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA	Moore B., Porat I., Overbeek R., Palmeri A., Rouse G.,
RA	Saenphitachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
RA	Leigh J.A.;
RT	"Complete genome sequence of the mesophilic hydrogenotrophic
RT	methanogen Methanococcus maripaludis.";
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL: BX957220, CAF30065.1; -
DR	GO: GO:0018493; F:formylmethanofuran dehydrogenase activity; IEA.
DR	GO: GO:0016491; F:oxidoreductase activity; IEA.
DR	InterPro: IPR011059; Meta10_hydro1ae.
KW	Complete proteome; Oxidoreductase.
SO	SEQUENCE 583 AA; 64594 MW; 76CF31FF5DA0263 CRC64;
QY	1 SASODISNYLN 11
DB	305 SKAEDISNYVN 315
RESULT 29	
CAF30065	PRELIMINARY; PRT; 956 AA.
ID	CAF30065
AC	CAF30065;
DT	03-MAR-2004 (TREMBlrel. 27, Created)
DT	03-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT	04-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE	Formylmethanofuran dehydrogenase, subunit A (BC 1.2.99.5).
GN	FMDA GN MWP0509.
OS	Methanococcus maripaludis.
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC	Methanococcaceae; Methanococcus.
OX	NCBI_TaxID=39152;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	STRAIN=S2 / LL;
RA	Hendrickson E.L., Kaul R., Zhou Y., Boyee D., Chapman P., Chung J.,
RA	Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA	Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA	Moore B., Porat I., Overbeek R., Palmeri A., Rouse G.,
RA	Saenphitachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
RA	Leigh J.A.;
RT	"Complete genome sequence of the mesophilic hydrogenotrophic
RT	methanogen Methanococcus maripaludis.";
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL: BX957220, CAF30065.1; -
DR	GO: GO:0018493; F:formylmethanofuran dehydrogenase activity; IEA.
DR	GO: GO:0016491; F:oxidoreductase activity; IEA.
DR	InterPro: IPR011059; Meta10_hydro1ae.
KW	Complete proteome; Oxidoreductase.
SO	SEQUENCE 583 AA; 64594 MW; 76CF31FF5DA0263 CRC64;
QY	1 SASODISNYLN 11
DB	305 SKAEDISNYVN 315
RESULT 30	
CAF30065	PRELIMINARY; PRT; 956 AA.
ID	CAF30065
AC	CAF30065;
DT	03-MAR-2004 (TREMBlrel. 27, Created)
DT	03-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT	04-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE	Formylmethanofuran dehydrogenase, subunit A (BC 1.2.99.5).
GN	FMDA GN MWP0509.
OS	Methanococcus maripaludis.
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC	Methanococcaceae; Methanococcus.

AC Q8ILX3; 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF14_0120;
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2285705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Bertram M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
RA Pereira M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrall B.,
RT "Genome sequence of the human malaria parasite Plasmodium
falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014817; AAN36732.1; -.
KW Hypothetical protein.
SQ SEQUENCE 956 AA; 112773 MW; D32D85CA78D40D5B CRC64;

Query Match 74.1%; Score 40; DB 2; Length 956;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASODISNTYN 11
Db 339 ASSTDISNTYN 349

RESULT 29
Q7RDE1 PRELIMINARY; PRT; 1116 AA.
AC Q7RDE1; 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PYO5481;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=17XNL;
RC PubMed=12368865;
RA Carlton J.M., Angiuoli S.V., Sub B.B., Kocif T.W., Pereira M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmiller S.B., Feldblum T.V.,
RA Cho J.K., Quackenbush J., Sedegh M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R., Ili, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Jance C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01001745; EAA17511.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1116 AA; 132831 MW; E24DA27C99E70495 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 1116;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SASODISNTYN 11
Db 339 NAKEDIDNTYN 349

RESULT 30
Q7KTP3 PRELIMINARY; PRT; 7500 AA.
AC Q7KTP3; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG18251-PC.
GN Name=Map-300; ORFNames=CG18251;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.R., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abail J.F., Abpayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burdick K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glisic A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Iobagwan C.,
RA Jalali M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasco P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tecior C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodgerter, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sedegh E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celisner S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AEO03608; AAS64640.1; -
DR InterPro; IPR000345; Cytochrome BS.
DR InterPro; IPR003900; KID Repeat.
DR InterPro; IPR011036; PH-related.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF02524; KID; 4.
DR Pfam; PF00435; Spectrin; 29.
DR SMART; SM00150; SPC; 44.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
SQ SEQUENCE 7500 AA; 861746 MW; 44477BA8FC38667B CRC64;
QY 1 SASQDISNTN 11
DB 6615 SISQDIESTYN 6625
Query Match 74.1%; Score 40; DB 2; Length 7500;
Best Local Similarity 72.7%; Pred. No. 1.4e+03;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
RESULT 31
AAS64640 PRELIMINARY; PRT; 7500 AA.
ID AAS64640
AC AAS64640;
DT 01-APR-2004 (TEMBLrel. 27, Created)
DT 01-APR-2004 (TEMBLrel. 27, Last sequence update)
DT 01-APR-2004 (TEMBLrel. 27, Last annotation update)
DE CG18251-PC.
MSP-300 OR CG18251.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10711132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abriil J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brocktein P., Brotier P.,
RA Burlis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Moadary C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleib J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Schaefer F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celisner S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleib J.M., Park S., Pfeiffer B.D., Richardson S., Sodegryn E.J.,
RA Svirskaas R., Taber P.B., Man K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [13]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [14]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celisner S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

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RN [6]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003608; AAS64640.1; -
SQ SEQUENCE 7500 AA; 861729 MW; 44477BA8FC36667B CRC64;

Query Match
Best Local Similarity 74.1%; Score 40; DB 2; Length 7500;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASODISNTYN 11
DB 6615 SLSDIESYLN 6625

RESULT 32
Q9VMT8 PRELIMINARY; PRT; 7735 AA.
ID Q9VMT8;
AC Q9VMT8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG18251-PB.
GN Name=Msp-300; ORFNames=CG18251;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxId=7227;
OK [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gockayne J.D.,
RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang M., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazef J.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch L., Baldwin D.,
RA Bailew R.M., Baeu A.V., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolnakov S.,
RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Diez S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferraz C., Gerhart W.M., Glasser K.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegam C.,
RA Jallali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matcel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlisina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,
RA Palczolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palzeto K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamis I., Simpson M., Skupki M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong M., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.

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RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.N., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertan B.P.,
RA Beilencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003608; AAF52223.3; -
DR HSSP; Q15149; IMB8.
DR IntAct; Q9VMT8; -.
DR FlyBase; FBgn0010070; Msp-300.
DR GO; GO:0007498; P:mesoderm development; NAS.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR000345; Cyt_c_heme_BS.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00435; Spectrin; 35.
DR SMART; SM00033; CH; 2.
DR SMART; SM00150; SPEC; 44.
DR PROSITE; PS50021; CH; 2.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN.1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN.1.
SQ SEQUENCE 7735 AA; 887874 MW; D3A2D5980B7C9D23 CRC64;

Query Match
Best Local Similarity 74.1%; Score 40; DB 2; Length 7735;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASODISNTYN 11
DB 6850 SLSDIESYLN 6860

RESULT 33
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
RL "Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain

```



```

DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4B843B9C5B577F16 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 107;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 25 ASODISSYLN 34

RESULT 34
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD5673.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

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Query Match 72.2%; Score 39; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 25 ASODISSYLN 34

RESULT 35
KVSH_MOUSE STANDARD; PRT; 117 AA.
ID KVSH_MOUSE
AC P016f1;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-V region MOPC 173B precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81064681; PubMed=6777049;
RA Max E.E., Seidman J.G., Miller H., Leder P.;
RT "Variation in the crossover point of kappa immunoglobulin gene V-J
RT recombination: evidence from a cryptic gene."
RL Cell 21:793-799(1980).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; K00880; AAA39031.1; -.
DR PIR; A01924; KVM53B.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 22
FT DOMAIN 23 117 IG kappa chain V-V region MOPC 173B.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 >117 Complementarity-determining-3.
FT DISUPRID 45 110 By similarity.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12954 MW; 24B3D4B9AC2B4D6C CRC64;

Query Match 72.2%; Score 39; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASODISNYLN 11
DB 47 ASODIHGYLN 56

RESULT 36
Q9X556 PRELIMINARY; PRT; 225 AA.
ID Q9X556;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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```

DE Cysteine aminopeptidase (Fragment).
GN Name=pepC;
OS Enterococcus faecium (Streptococcus faecium).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1352;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BFE 900;
RX MEDLINE=99240446; PubMed=10224016;
RA Franz C.M.A.P., Worobo R.W., Quadri L.E.N., Schillinger U.,
  Holzapfel W.H., Vederas J.C., Stiles M.E.;
RT "Atypical genetic locus associated with constitutive production of
  enterocin B by Enterococcus faecium BFE 900."
RL Appl. Environ. Microbiol. 65:2170-2178(1999).
DR EMBL: AF121254; MADS28219.1; -.
DR MEROPS: C01.066; -.
DR GO: GO:0004177; F:aminopeptidase activity; IEA.
DR GO: GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR004134; Peptidase C1B.
DR InterPro: IPR000169; Pept_cys_acste.
DR Pfam: PF03051; Pept_C1-like; 1.
DR PROSITE: PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.
KM AminoPeptidase.
FT NON_TER 225
SQ SEQUENCE 225 AA; 25625 MW; 194451D51DF51C56 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 225;
Best Local Similarity 63.6%; Pred. No. 50;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
DB 166 SNSRDJNNYLN 176

RESULT 37
Q838Y1 PRELIMINARY; PRT; 461 AA.
AC Q838Y1;
DT 01-JUN-2003 (TRENBLREL. 24, Created)
DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE AminoPeptidase C.
GN Name=pepC; OrderedLocusNames=EF0302;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550657; PubMed=1263927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
  Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
  Teichlin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
  Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
  Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
  Khouri H.M., Uettermann T.R., Radune D., Ketchum K.A., Dougherty B.A.,
  Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
  Enterococcus faecalis."
RL Science 299:2071-2074(2003).
DR EMBL: AE016947; AAO80165.1; -.
DR HSSP: Q13867; 2CBS.
DR MEROPS: C01.066; -.
DR TIGR: EF0302; -.
DR GO: GO:0004177; F:aminopeptidase activity; IEA.
DR GO: GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR004134; Peptidase C1B.
DR InterPro: IPR000169; Pept_cys_acste.
DR Pfam: PF03051; Pept_C1-like; 1.
DR PIRSF: PIRSF005700; PepC; 1.

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DR PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
KM AminoPeptidase; Complete proteome.
SQ SEQUENCE 461 AA; 52197 MW; 0B7FA885E60EE008 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 461;
Best Local Similarity 63.6%; Pred. No. 11e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASODISNYLN 11
DB 166 SNSRDJNNYLN 176

RESULT 38
Q9H192 PRELIMINARY; PRT; 506 AA.
AC Q9H192;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Hypothetical protein Tal450.
GN OrderedLocusNames=Tal450;
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
  Mewes H.-W., Fishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermophilic scavenger Thermoplasma
  acidophilum."
RL Nature 407:508-513(2000).
DR EMBL: AL445067; CAC12570.1; -.
DR GO: GO:0003824; P:catalytic activity; IEA.
DR GO: GO:0008152; P:metabolic activity; IEA.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 3.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 506 AA; 55694 MW; 88DED97D384EC915 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 506;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASODISNYLN 10
DB 202 SSIQDISNYLN 211

RESULT 39
Q8EV69 PRELIMINARY; PRT; 1093 AA.
AC Q8EV69;
DT 01-MAR-2003 (TRENBLREL. 23, Created)
DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Hypothetical protein MYP66990.
GN OrderedLocusNames=MYP66990;
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=1246555;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
  Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an
  intracellular bacterial pathogen in humans."

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RL Nucleic Acids Res. 30:5293-5300(2002).
 DR EMBL; AP004173; BAC44491.1; -
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 1093 AA; 119056 MM; 3F2373983DC1CF79 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 1093;
 Best Local Similarity 54.5%; Pred. No. 2.7e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SASODISNYLN 11
 Db 640 SSEDVSOYIN 650

RESULT 40

07PDL3 PRELIMINARY; PRT; 1665 AA.
 AC 07PDL3;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, last annotation update)
 DE Erythrocyte membrane protein PFEMP3.
 GN Name=PY06125;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=12368865;
 RA Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Sengenut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldlyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
 RA Florens L., Yates F.R., III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdiva A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01002038; EAA18281.1; -
 SQ SEQUENCE 1665 AA; 191206 MM; 03BB304FF802057C CRC64;

Query Match 72.2%; Score 39; DB 2; Length 1665;
 Best Local Similarity 70.0%; Pred. No. 4.2e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ASODISNYLN 11
 Db 305 SEDDIENYLN 314

Search completed: December 17, 2004, 19:14:40
 Job time : 34.8764 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 17, 2004, 18:10:02 ; Search time 21.2753 Seconds
(without alignments)
118.029 Million cell updates/sec

Title: US-10-089-500-7

Perfect score: 37

Sequence: 1 YSSNLS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: geneeqp1980s:*\n2: geneeqp1990s:*\n3: geneeqp2000s:*\n4: geneeqp2001s:*\n5: geneeqp2002s:*\n6: geneeqp2003as:*\n7: geneeqp2003bs:*\n8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	37	100.0	7 4 AAB81983	Aab81983 Gangliosid
2	37	100.0	7 6 ABU11008	Abu11008 Modified
3	37	100.0	108 4 AAB81988	Aab81988 Gangliosid
4	37	100.0	108 4 AAB81986	Aab81986 Gangliosid
5	37	100.0	108 4 AAB81990	Aab81990 Gangliosid
6	37	100.0	108 6 ABU11011	Abu11011 Modified
7	37	100.0	108 6 ABU11013	Abu11013 Modified
8	37	100.0	128 2 AAR33257	Aar33257 Rat Immun
9	37	100.0	128 2 AAR53340	Aar53340 KM641 H c
10	37	100.0	128 2 AAY28368	Aay28368 PM6641 LA
11	37	100.0	128 3 AAB01628	Aab01628 Murine im
12	37	100.0	128 4 AAB81994	Aab81994 Gangliosid
13	37	100.0	128 4 AAB81995	Aab81995 Gangliosid
14	37	100.0	128 4 AAB81997	Aab81997 Gangliosid
15	37	100.0	128 4 AAB81978	Aab81978 Gangliosid
16	37	100.0	128 4 AAB81966	Aab81966 Gangliosid
17	37	100.0	128 4 AAB81989	Aab81989 Gangliosid
18	37	100.0	128 4 AAB81993	Aab81993 Gangliosid
19	37	100.0	128 4 AAB81992	Aab81992 Gangliosid
20	37	100.0	128 4 AAB81998	Aab81998 Gangliosid
21	37	100.0	128 6 ABU11003	Abu11003 Modified
22	34	91.9	273 3 AAR52865	Aar52865 Anti-infl
23	34	91.9	744 7 ADE62374	Ade62374 Rat Prote
24	33	89.2	368 5 AAB55521	Abb55521 Lactococc
25	33	89.2	474 2 AAY23802	Aay23802 A gyrase

26	32	86.5	36 3 AAY69824	Aay69824 HIV-1 gp4
27	32	86.5	36 8 ADO10396	Ado10396 HIV1 gIyc
28	32	86.5	481- 5 ABB93504	Abb93504 Herbicida
29	32	86.5	500 7 ADD14911	Add14911 N. tabacu
30	31	83.8	277 6 ABU25460	Abu25460 Protein e
31	31	83.8	347 3 AAY97205	Aay97205 Campyloba
32	31	83.8	347 6 ABB18486	Abj18486 Campyloba
33	31	83.8	380 6 ABB80364	Abp80364 N. gonorr
34	30	81.1	14 4 AAM97437	Aam97437 Human pep
35	30	81.1	23 6 ABO12747	Abol12747 Human zin
36	30	81.1	56 5 ABR03340	Abp03340 Human ORF
37	30	81.1	83 4 AAY59057	Aay59057 Propionib
38	30	81.1	83 6 ABB55576	Abm55576 Propionib
39	30	81.1	167 6 ABU27913	Abu27913 Protein e
40	30	81.1	182 3 AAG49871	Aag49871 Arabidops
41	30	81.1	182 3 AAG24379	Aag24379 Arabidops
42	30	81.1	196 3 AAG49870	Aag49870 Arabidops
43	30	81.1	196 3 AAG24378	Aag24378 Arabidops
44	30	81.1	211 6 ABU33502	Abu33502 Protein e
45	30	81.1	213 3 AAG49869	Aag49869 Arabidops

ALIGNMENTS

RESULT 1
AAB81983
ID AAB81983 standard; peptide; 7 AA.
AC AAB81983;
DT 03-JUL-2001 (first entry)
XX Ganglioside GD3 specific antibody related peptide SEQ ID NO: 7.
DE Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX Mus musculus.
XX WO200123432-A1.
XX 05-APR-2001.
XX 29-SEP-2000; 2000WO-JP006774.
XX PF 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI, 2001-266143/27.
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX Claim 4; Page 142; 183pp; Japanese.
XX The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumors, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX Sequence 7 AA;
Query Match 100.0%; Score 37; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
 |||||
 DB 1 YSSNLS 7

RESULT 2

ABU11008
 ID ABU11008 standard; peptide; 7 AA.

AC AAB11008;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated peptide #5.

KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

OS Mus musculus.

PN WO200278739-A1.

PD 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Shitara K, Niwa R, Kanazawa J, Asada M;

DR WPI; 2003-067410/06.

PT Drugs containing genetically-modified antibody against ganglioside GD3, its fragment, immunocompetent cell activators or/and antitumor agents in combination, applicable in treating malignant tumor like melanoma.

PS Claim 6; Page 99; 121pp; Japanese.

CC The invention describes drugs contain a genetically-modified antibody against ganglioside GD3 or its fragment and at least 1 of a substance capable of activating immunocompetent cells and a substance having an antitumor activity in combination. The drugs can be used to treat tumour CC like melanoma and can provide a treatment with enhanced therapeutic effect and little side-reactions, particularly to relieve problems of CC side-effects during the conventional single administration. This sequence CC represents a peptide associated with the anti- ganglioside GD3 antibody

XX Sequence 7 AA;

Query Match 100.0%; Score 37; DB 6; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
 |||||
 DB 1 YSSNLS 7

RESULT 3

AAB81988
 ID AAB81988 standard; protein; 108 AA.

AC AAB81988;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody; cancer.

OS Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI; 2001-266143/27.

PT New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

PS Claim 22; Page 172-173; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react CC specifically with ganglioside GD3. The antibody and its derivatives are CC useful in the diagnosis and therapy of tumours, particularly cancer CC diagnosis. The present sequence is a protein used in the exemplification CC of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 37; DB 4; Length 108;

Best Local Similarity 100.0%; Pred. No. 9.1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
 |||||
 DB 50 YSSNLS 56

RESULT 4

AAB81986
 ID AAB81986 standard; protein; 108 AA.

AC AAB81986;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody; cancer.

OS Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI; 2001-266143/27.

PT New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

XX Example 1; Page 143-144; 183pp; Japanese.

PS The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 37; DB 4; Length 108;

Best Local Similarity 100.0%; Pred. No. 9.1; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
|||||
DB 50 YSSNLHS 56

RESULT 5

AB081990 AAB81990 standard; protein; 108 AA.

XX AAB81990;

XX 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Mus musculus.

XX WO200123432-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

XX 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody

XX and derivatives against ganglioside GD3; useful in diagnosis and therapy

XX of e.g. tumors, with low antigenicity, little side effects but potent

XX activity in cancer.

XX Claim 11; Page 174-175; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react

XX specifically with ganglioside GD3. The antibody and its derivatives are

XX useful in the diagnosis and therapy of tumors, particularly cancer

XX diagnosis. The present sequence is a protein used in the exemplification

XX of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 37; DB 4; Length 108;

Best Local Similarity 100.0%; Pred. No. 9.1; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
|||||

DB 50 YSSNLHS 56

RESULT 6

AB011011 AAB11011 standard; protein; 108 AA.

XX AAB11011;

XX 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #4.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Synthetic.

XX WO200278739-A1.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-JP003170.

XX 29-MAR-2001; 2001JP-00097483.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3, in

XX its fragment, immunocompetent cell activators or/and anticancer agents in

XX combination, applicable in treating malignant tumor like melanoma.

XX Claim 8; Page 100; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody

XX against ganglioside GD3 or its fragment and at least 1 of a substance

XX capable of activating immunocompetent cells and a substance having an

XX antitumor activity in combination. The drugs can be used to treat tumour

XX like melanoma and can provide a treatment with enhanced therapeutic

XX effect and little side-reactions, particularly to relieve problems of

XX side-effects during the conventional single administration. This sequence

XX represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 108 AA;

Query Match 100.0%; Score 37; DB 6; Length 108;

Best Local Similarity 100.0%; Pred. No. 9.1; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
|||||

DB 50 YSSNLHS 56

RESULT 7

AB011013 AAB11013 standard; protein; 108 AA.

XX AAB11013;

XX 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #6.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Mus musculus.

XX WO200278739-A1.

XX

```

PD 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-JP003170.
XX
XX 29-MAR-2001; 2001JP-00097483.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Niwa R, Kanazawa J, Asada M,
XX
XX WPI; 2003-067410/06.
XX
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX
XX Claim 7; Page 113; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumour
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 108 AA;
SQ
Query Match 100.0%; Score 37; DB 6; Length 108;
Best Local Similarity 100.0%; Pred.No.9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLSHS 7
Db 50 YSSNLSHS 56
RESULT 8
AAR33257
ID AAR33257 standard; protein; 128 AA.
XX
XX AAR33257;
AC
XX
XX 25-MAR-2003 (revised)
DT 12-JUL-1993 (first entry)
XX
XX Rat immunoglobulin L chain variable region of pKM641LA2.
DE
XX
XX Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
KW humanised; chimeric; antibody; expression vector.
XX
XX Rattus rattus.
OS
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX Protein /note="Signal peptide"
XX /note="Mature protein"
XX
XX EP53199-A2.
XX
XX 24-MAR-1993.
XX
XX 18-SEP-1992; 92EP-00116026.
XX
XX 18-SEP-1991; 91JP-00238375.
XX
XX (KYOW ) KYOWA HAKKO KOGYO CO LTD.
XX
XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX
XX WPI, 1993-095510/12.

```

```

DR N-PSDB; AAQ33258.
XX
XX Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
XX cancers, such as melanoma, neuroblastoma, etc.
XX
XX Claim 6; Page 30-31; 63pp; English.
XX
XX The sequences given in AAR33256-57 represent rat heavy and light chain
XX variable regions respectively. The DNA sequences encoding these proteins
XX were used in the construction of humanised chimeric antibody expression
XX vectors. In these humanised antibodies none of the amino acids of the non
XX -human animal Ab variable region have been changed. (Updated on 25-MAR-
XX 2003 to correct FN field.)
XX
XX Sequence 128 AA;
SQ
Query Match 100.0%; Score 37; DB 2; Length 128;
Best Local Similarity 100.0%; Pred.No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLSHS 7
Db 70 YSSNLSHS 76
RESULT 9
AAR53340
ID AAR53340 standard; protein; 128 AA.
XX
XX AAR53340;
AC
XX
XX 18-NOV-1994 (first entry)
DT
XX
XX KM641 H chain variable region.
DE
XX
XX Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
KW expression vector; heavy; light; chain; hypervariable region; CDR;
KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX
XX Mus musculus.
OS
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX /label= sig_peptide
XX
XX AU9346181-A.
XX
XX 17-MAR-1994.
XX
XX 07-SEP-1993; 93AU-00046181.
XX
XX 07-SEP-1992; 92JP-00238452.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
XX
XX WPI; 1994-126857/16.
XX
XX N-PSDB; AAQ45438.
XX
XX Humanised antibody specific for ganglioside GM2 - used for producing a
XX cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX
XX Example 2; Page 115-116; 191pp; English.
XX
XX Example 2 describes the construction of the vector pCHI641HA1 for
XX chimeric human antibody H chain expression. mRNA from mouse anti-GD3
XX monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
XX cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
XX chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
XX AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
XX was constructed by joining the H chain variable region gene from
XX pKM641HA3 to a vector for chimeric human Ab H chain expression using the

```

CC synthetic DNAe given in AAG63439 and AAG63440
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 37; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
| | | | |
DB 70 YSSNLS 76

RESULT 10
AAY28368
ID AAY28368 standard; protein; 128 AA.

XX AAY28368;
DT 04-NOV-1999 (first entry)

XX PKM641 LA2 immunoglobulin light chain.

XX antibody; nucleotide; genomic; hypervariable region; chimeric;
KW light chain; amino acid.

XX Mus sp.

XX US5939532-A.

XX 17-AUG-1999.

XX 07-JUN-1995; 95US-00483528.

XX 07-SEP-1993; 93US-00116778.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;

XX WPI; 1999-468416/39.

XX N-PSDB; AAX9481.

XX Chimeric human antibody expression vectors.

XX Example 1; Col 99; 188pp; English.

XX This immunoglobulin region was isolated from PKM641LA2.A methionine
CC codon, presumably the initiation codon ATG, was found in the vicinity of
CC the 5' terminus and the sequence has a full length leader sequence. The
CC chimeric human antibodies are useful in the treatment of cancer,
CC especially that which is of neural ectodermal origin. In contrast to
CC prior art constructs based on mouse monoclonal antibodies, the chimeric
CC human antibodies do not cause anti-mouse immunoglobulin production. The
CC chimeric human antibodies have a prolonged half-life and a reduced
CC frequency of adverse effects when compared to mouse monoclonal antibodies
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 37; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
| | | | |
DB 70 YSSNLS 76

RESULT 11
AAB01628
ID AAB01628 standard; protein; 128 AA.
XX
XX AAB01628;

XX 07-DEC-2000 (first entry)
DT
XX Murine immunoglobulin light chain variable region.
DE
XX Mouse; immunoglobulin; L chain; light chain; variable region; cancer;
KW humanised antibody.
XX
XX Mus sp.

OS

PH Key Location/Qualifiers

FT Peptide 1..20 /label= signal_peptide

FT Protein 21..128 /label= mature_immunoglobulin_light_chain_V_region

XX EP1013761-A2.

XX 28-JUN-2000.

XX 18-SEP-1992; 99EP-00124345.

XX 18-SEP-1991; 91JP-0028375.

XX 18-SEP-1992; 92EP-00116026.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;

XX WPI; 2000-402204/35.

XX N-PSDB; AAA51004.

XX New humanized chimera antibody KM-871 useful for treating cancer,
PT comprises variable region of mouse monoclonal antibody, reactive with
PT ganglioside and human antibody constant region.

XX Claim 14; Page 28-29; 65pp; English.

XX The present sequence is a murine immunoglobulin light chain variable
CC region from plasmid KM-641. The coding sequence was used in the creation
CC of an expression vector, along with the sequence for a human antibody, to
CC produce humanised chimaeric antibodies, which can be used to treat
CC cancer. Humanised chimaeric antibodies are more effective than mouse
CC antibodies as they do not provoke a reaction in the human and side
CC effects, such as the formation of anti-mouse immunoglobulin antibody and
CC the rapid half-life of the immunoglobulins, do not occur
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 37; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
| | | | |
DB 70 YSSNLS 76

RESULT 12
AAB81994
ID AAB81994 standard; protein; 128 AA.

XX AAB81994;

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein #3.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

XX cancer.

XX Synthetic.

PN WO200123432-A1.
XX
XX PD 05-APR-2001.
XX
XX PF 29-SEP-2000; 2000WO-JP006774.
XX
XX PR 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX DR WPI; 2001-266143/27.
XX DR N-PSDB; AAF86898.
XX
XX PT New human type complementation-determining region-transplanted antibody
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX PT of e.g. tumors, with low antigenicity, little side effects but potent
XX PT activity in cancer.
XX
XX PS Example 1; Page 155-156; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
XX CC specifically with ganglioside GD3. The antibody and its derivatives are
XX CC useful in the diagnosis and therapy of tumours, particularly cancer
XX CC diagnosis. The present sequence is a protein used in the exemplification
XX CC of the invention
XX
XX SQ Sequence 128 AA;
SQ
QY Query Match 100.0%; Score 37; DB 4; Length 128;
QY Best Local Similarity 100.0%; Pred. No. 11;
QY Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLSHS 7
QY 70 YSSNLSHS 76
DB
RESULT 13
ID AAB81995
ID AAB81995 standard; protein; 128 AA.
XX
XX AC AAB81995;
XX
XX DT 03-JUL-2001 (first entry)
XX
XX DE Ganglioside GD3 specific antibody related protein #4.
XX
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX KW cancer.
XX
XX OS Synthetic.
XX
XX PN WO200123432-A1.
XX
XX PD 05-APR-2001.
XX
XX PF 29-SEP-2000; 2000WO-JP006774.
XX
XX PR 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX DR WPI; 2001-266143/27.
XX DR N-PSDB; AAF86901.
XX
XX PT New human type complementation-determining region-transplanted antibody
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent
XX PT activity in cancer.
XX
XX PS Example 1; Page 157-158; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
XX CC specifically with ganglioside GD3. The antibody and its derivatives are
XX CC useful in the diagnosis and therapy of tumours, particularly cancer
XX CC diagnosis. The present sequence is a protein used in the exemplification
XX CC of the invention
XX
XX SQ Sequence 128 AA;
SQ
QY Query Match 100.0%; Score 37; DB 4; Length 128;
QY Best Local Similarity 100.0%; Pred. No. 11;
QY Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLSHS 7
QY 70 YSSNLSHS 76
DB
RESULT 14
ID AAB81997
ID AAB81997 standard; protein; 128 AA.
XX
XX AC AAB81997;
XX
XX DT 03-JUL-2001 (first entry)
XX
XX DE Ganglioside GD3 specific antibody related protein #6.
XX
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX KW cancer.
XX
XX OS Synthetic.
XX
XX PN WO200123432-A1.
XX
XX PD 05-APR-2001.
XX
XX PF 29-SEP-2000; 2000WO-JP006774.
XX
XX PR 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX DR WPI; 2001-266143/27.
XX DR N-PSDB; AAF86907.
XX
XX PT New human type complementation-determining region-transplanted antibody
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX PT of e.g. tumors, with low antigenicity, little side effects but potent
XX PT activity in cancer.
XX
XX PS Example 1; Page 161-162; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
XX CC specifically with ganglioside GD3. The antibody and its derivatives are
XX CC useful in the diagnosis and therapy of tumours, particularly cancer
XX CC diagnosis. The present sequence is a protein used in the exemplification
XX CC of the invention
XX
XX SQ Sequence 128 AA;
SQ
QY Query Match 100.0%; Score 37; DB 4; Length 128;
QY Best Local Similarity 100.0%; Pred. No. 11;
QY Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLSHS 7

DB 70 YSSNLSHS 76

RESULT 15

AAB81978 standard; protein; 128 AA.

AC AAB81978;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KM cancer.

OS Mus musculus.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI; 2001-266143/27.

PT New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

PS Example 1; Page 140; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumors, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

CC of the invention

CC Sequence 128 AA;

Query Match 100.0%; Score 37; DB 4; Length 128;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7

DB 70 YSSNLSHS 76

RESULT 16

AAB81996 standard; protein; 128 AA.

AC AAB81996;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #5.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KM cancer.

OS Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI; 2001-266143/27.

DR N-PSDB; AAF86904.

PT New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

PS Example 1; Page 159-160; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumors, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

CC Sequence 128 AA;

Query Match 100.0%; Score 37; DB 4; Length 128;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7

DB 70 YSSNLSHS 76

RESULT 17

AAB81999 standard; protein; 128 AA.

AC AAB81999;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #8.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KM cancer.

OS Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI; 2001-266143/27.

DR N-PSDB; AAF86913.

PT New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy

XX WO200123432-A1.
 XX
 XX 05-APR-2001.
 PD
 XX 29-SEP-2000; 2000WO-JP006774.
 PF
 XX 30-SEP-1999; 99JP-00278291.
 PR 06-APR-2000; 2000JP-00105088.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 PI
 XX WPI; 2001-266143/27.
 DR
 XX N-PSDB; AAR6912.
 DR
 XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 PS Example 3; Page 164-165; 183pp; Japanese.
 CC
 XX The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 CC
 XX Sequence 128 AA;
 SQ

Query Match 100.0%; Score 37; DB 4; Length 128;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSNLS 7
 DB 70 YSSNLS 76

RESULT 21
 ID ABU11003 standard; protein; 128 AA.
 XX
 XX ABU11003;
 AC
 XX 04-FEB-2003 (first entry)
 DT
 XX Modified ganglioside GD3 antibody associated protein #2.
 DE
 XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 XX
 XX Mus musculus.
 OS
 XX WO200278739-A1.
 PN
 XX 10-OCT-2002.
 PD
 XX 29-MAR-2002; 2002WO-JP003170.
 PF
 XX 29-MAR-2001; 2001JP-00097483.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Shitara K, Niwa R, Kanazawa J, Asada M;
 PI
 XX WPI; 2003-067410/06.
 DR
 XX Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX

PS Example 3; Page 98; 121pp; Japanese.
 XX
 XX The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 CC
 XX Sequence 128 AA;
 SQ

Query Match 100.0%; Score 37; DB 6; Length 128;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSNLS 7
 DB 70 YSSNLS 76

RESULT 22
 ID AAR52865 standard; protein; 273 AA.
 XX
 XX AAR52865;
 AC
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 09-SEP-1994 (first entry)
 XX
 XX Anti-Influenza N10 scFv.
 DE
 XX Monoclonal antibody N10; target binding polypeptide; scFv; scFv;
 XX single chain antibody; protein secretion; FLAG; Escherichia coli;
 XX antibody engineering; humanized antibody; Influenza virus; neuraminidase.
 XX

Unidentified.
 OS
 XX
 XX Key Location/Qualifiers
 FH 1..22
 FT Peptide /label= Sig_peptide
 FT 266..273
 FT Peptide /note="C-terminal FLAG tail"
 FT

PN WO9407921-A1.
 XX
 XX 14-APR-1994.
 PD
 XX 24-SEP-1993; 93WO-AU000491.
 PF
 XX 25-SEP-1992; 92AU-00004973.
 PR
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA
 XX Hudson PJ, Lah M, Kortt A, Irving RA, Atwell JL, Malby RL;
 PI Power BE, Colman PM;
 PI
 XX WPI; 1994-135515/16.
 DR
 XX N-PSDB; AAG62957.
 DR
 XX New target-binding polypeptide(s) used for diagnosis, etc. - having a
 PT stable core polypeptide region with at least one target-binding region
 PT covalently attached, opt. mutated to alter specificity, etc.
 PT
 XX Disclosure; Page 41; 67pp; English.
 PS
 XX An scFv fragment of NC10 (a monoclonal antibody that recognises influenza
 CC virus N9 neuraminidase) was expressed in Escherichia coli. The N-terminal
 CC PeB signal peptide directed the scFv fragment into the periplasm where
 CC it became associated with the insoluble membrane fraction. An octapeptide
 CC FLAG tail was fused to the C-terminus of scFv and used to monitor scFv

CC during purification. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
XX
SQ Sequence 273 AA;
Query Match 91.9%; Score 34; DB 2; Length 273;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 YSSNLS 7
DB 208 YTSNLS 214
RESULT 23
ADE62374
ID ADE62374 standard; protein; 744 AA.
XX ADE62374;
XX
XX 29-JAN-2004 (first entry)
XX
XX DE Rat Protein AAB60512, SEQ ID NO 8303.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX MO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002MO-US025765.
XX
XX 14-AUG-2001; 2001US-0312447P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-033347P.
XX
XX (GHEO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX GENBANK; AAB60512.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 744 AA;
Query Match 91.9%; Score 34; DB 7; Length 744;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 YSSNLS 7
DB 501 YSSNLS 507
RESULT 24
ABB55521
ID ABB55521 standard; protein; 368 AA.
XX ABB55521;
XX
XX 29-AUG-2003 (revised)
XX
XX DT 16-MAY-2002 (first entry)
XX
XX DE Lactococcus lactis protein yweB.
XX
XX Lactococcus lactis; IL1403.
XX
XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX
XX Lactococcus lactis; IL1403.
XX
XX FR2807446-A1.
XX
XX 12-OCT-2001.
XX
XX 11-APR-2000; 2000FR-00004630.
XX
XX 11-APR-2000; 2000FR-00004630.
XX
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;
XX
XX WPI; 2002-043418/06.
XX
XX New nucleotide sequence useful in the identification or Lactococcus
XX lactis and related species.
XX
XX Claim 6; SEQ ID NO 2223; 2504pp; French.
XX
XX The present invention is related to a Lactococcus lactis nucleotide
XX sequence (ABA90521) and related proteins (ABB53300-ABB5621). The nucleic
XX acid sequence is useful in the detection and/or amplification of nucleic
XX acid sequence, particularly to identify Lactococcus lactis or related
XX species. The proteins of the invention are useful for the biosynthesis or
XX biodegradation of a composition of interest. The invention helps research
XX in lactic bacteria, particularly useful in the production of yogurt and
XX cheese. Note: The sequence data for this patent is based on equivalent
XX patent WO200177334 (published 18-OCT-2001) which is available in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to
XX standardise OS field)
XX
XX SQ Sequence 368 AA;
Query Match 89.2%; Score 33; DB 5; Length 368;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 YSSNLS 7

Db 121 FSSNLHS 127

RESULT 25

ID AAY23802 standard; protein; 474 AA.

AC AAY23802;

DT 14-SEP-1999 (first entry)

DE A gyrase protein sequence.

KW Identification; detection; microbe; gyrase gene; gyrase protein.

XX Unidentified.

XX JP11169175-A.

XX 29-JUN-1999.

XX 12-DEC-1997; 97JP-00343316.

XX 12-DEC-1997; 97JP-00343316.

PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.

DR WPI; 1999-422615/36.

DR N-PSDB; AAX86009.

PT Identification and detection of a microbe - by detection of a gyrase gene.

PS Example 12; Page 31-32; 42pp; Japanese.

CC The specification describes a method for the identification or detection of a microbe, using the gyrase gene as the index. The method involves the use of PCR primers to amplify DNA from the microbe, which is then

CC identified or detected depending on its base sequence. The method can be used to classify and identify an unidentified microbe strain rapidly and

CC with high precision. The present sequence represents a gyrase protein

CC Sequence 474 AA;

Query Match 89.2%; Score 33; DB 2; Length 474;

Best Local Similarity 85.7%; Pred. No. 3.1e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 0;

OY 1 YSSNLHS 7

Db 164 YSSNLHS 170

RESULT 26

ID AAY69824 standard; peptide; 36 AA.

AC AAY69824;

DT 20-APR-2000 (first entry)

DE HIV-1 gp41 envelope protein amino acids 628-663 mutant 2.

KW Cytostatic; human immunodeficiency virus gp41 envelope protein; antibody; antiviral; vaccine; human; pathogenic retrovirus; immunodominant zone;

KW immune response; mutein.

OS Human immunodeficiency virus 1.

XX Synthetic.

XX FR2771011-A1.

PD 21-MAY-1999.

XX 17-NOV-1997; 97PR-00014387.

XX 17-NOV-1997; 97PR-00014387.

PA (HIP-) HIPPOCAMPE SA.

PI Serres PF, Geurjon C, Deleage G, Combet C;

DR WPI; 2000-099991/09.

PT Vaccine against retroviral infection containing modified envelope protein.

PS Claim 4; Page 31; 37pp; French.

CC This sequence corresponds to a mutant of amino acids 628-663 of the gp41 envelope protein of the human immunodeficiency virus type 1 (HIV-1). The

CC invention relates to the generation of vaccine against the effects of infection, in humans or animals, and comprises a modified polypeptide

CC containing at least part of an envelope protein of a pathogenic retrovirus. The polypeptide can enter a target cell via a membrane

CC receptor for a host protein. The part of the envelope protein includes at least a fragment of an immunodominant zone and contains at least one

CC amino acid that is conserved in the immunodominant zone and present in the pathogenic retroviral strain. When unmodified, the polypeptide

CC induces an immune response against both the immunodominant zone and the host protein, and the modified polypeptide induces such a response

CC against the immunodominant zone only. The vaccines are particularly used to protect against human or feline immune deficiency viruses. The

CC modified polypeptide may also be used to raise specific antibodies for treatment of retroviral infections, particularly in the early stages

CC

SQ Sequence 36 AA;

Query Match 86.5%; Score 32; DB 3; Length 36;

Best Local Similarity 71.4%; Pred. No. 28; Mismatches 5; Conservative 2; Indels 0; Gaps 0;

Matches 16 YTSNIHS 22

OY 1 YSSNLHS 7

Db 16 YTSNIHS 22

AD010396 standard; peptide; 36 AA.

AC AD010396;

DT 01-JUL-2004 (first entry)

DE HIV1 glycoprotein 41 (gp41) mutant peptide #28.

KW HIV1; glycoprotein 41; gp41; retrovirus; membrane receptor; immune response; envelope protein; retroviral infection; HIV infection;

KW HIV infection; anti-HIV; virucide; cytokine; mutant; mutein.

OS Human immunodeficiency virus 1.

XX Synthetic.

XX US2004014046-A1.

XX 22-JAN-2004.

XX 22-JUL-2002; 2002US-00198938.

XX 22-JUL-2002; 2002US-00198938.

PA (MYME-) MYMETICS SA.

PI Serres PF;

XX WPI; 2004-121552/12.
XX
XX
XX Obtaining vaccines for preventing pathogenic effects of a retroviral
PT (e.g. HIV) infection in a host comprises selecting a modified polypeptide
PT that induces an immune response against the immunodominant region of an
PT envelope protein.
XX
XX
XX Example 3; Page 14; 17pp; English.
XX
XX The invention relates to a method of searching for and obtaining a
CC vaccine against pathogenic effects related to infection of an animal or
CC human host by a retrovirus capable of penetrating into a target cell of
CC the host, the target cell possessing a membrane receptor for a protein of
CC the host, comprising selecting as the vaccine a modified polypeptide that
CC induces an immune response directed against the immunodominant region of
CC an envelope protein and not against a protein of the host. The invention
CC also relates to a vaccine obtained by the method, an antibody obtained by
CC immunising a host with the aid of the vaccine, where the antibody
CC recognises the envelope protein and not the protein of the host and a
CC pharmaceutical composition containing the antibody. The method is useful
CC in obtaining vaccines for preventing the pathogenic effects related to a
CC retroviral (e.g. HIV or FIV) infection. This sequence represents an HIV1
CC glycoprotein 41 (gp41) mutant peptide used in the scope of the invention.
XX
SQ Sequence 36 AA;
XX
Query Match 86.5%; Score 32; DB 8; Length 36;
Best Local Similarity 71.4%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 YSSNLHS 7
Db |||:||||
16 YTSNIHS 22
XX
RESULT 28
ABB93504
ID ABB93504 standard; protein; 481 AA.
XX
XX ABB93504;
AC
XX
XX 31-MAY-2002 (first entry)
DT
XX
XX Herbicidally active polypeptide SEQ ID NO 2715.
DE
XX
XX Herbicidal; plant; agriculture; herbicide.
KM
XX
XX Arabidopsis thaliana.
OS
XX
XX WO200210210-A2.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 28-AUG-2001; 2001WO-EP009892.
PF
XX
XX 28-AUG-2001; 2001WO-EP009892.
PR
XX
XX (FARB) BAYER AG.
PA
XX
XX Tietjen K, Weidler M;
PI
XX
XX WPI; 2002-269010/31.
DR
XX
XX Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.
XX
XX Claim 5; SEQ ID NO 2715; 261pp + Sequence Listing; English.
PS
XX
XX The invention relates to identifying target proteins (ABB90790-ABB94016)
CC for herbicidally active compounds, comprising aligning and comparing

CC nucleic acid or amino acid sequences from plant with nucleic acid or
CC amino acid sequences from non-plant organisms using suitable search
CC parameters, where plant sequences having an E-value greater by a factor
CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides
XX
XX
SQ Sequence 481 AA;
XX
Query Match 86.5%; Score 32; DB 5; Length 481;
Best Local Similarity 85.7%; Pred. No. 51e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 YSSNLHS 7
Db |||:||||
6 YSSSLHS 12
XX
RESULT 29
ADD14911
ID ADD14911 standard; protein; 500 AA.
XX
XX ADD14911;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX N. tabacum Ntcel2 protein.
DE
XX
XX Tobacco; cyst and root knot nematode responsive promoter; promoter;
KM endo-1,4-beta-glucanase; ECase; Ntcel17; nematode; plant; Ti plasmid;
KM microparticle; ballistic transformation; protoplast; transgenic plant;
KM insecticidal protein; crystal protein; toxic; insect; dicot; monocot;
KM Ntcel2; enzyme.
XX
XX Nicotiana tabacum.
OS
XX
XX US2003106092-A1.
PN
XX
XX 05-JUN-2003.
PD
XX
XX 02-OCT-2001; 2001US-00970367.
PF
XX
XX 02-OCT-2001; 2001US-00970367.
PR
XX
XX (DAVI/) DAVIS E L.
PA (GOEL/) GOELLNER M.
XX
XX Davis E., Goellner M;
PI
XX
XX WPI; 2003-810836/76.
DR N-PSDB; ADD14910.
DR
XX
XX Nucleic acid construct for controlling cyst and root knot nematodes,
PT comprising a cyst and root knot nematode responsive promoter and
PT optionally a heterologous nucleic acid.
XX
XX
PS Disclosure; SEQ ID NO 2; 32pp; English.
XX
XX The invention discloses a nucleic acid construct comprising, in the 5' to
CC 3' direction, a cyst and root knot nematode responsive promoter and,
CC optionally, a heterologous nucleic acid positioned downstream from the
CC promoter. The cyst and root knot nematode responsive promoter preferably
CC comprises the Nicotiana endo-1,4-beta-glucanase (ECase), Ntcel17, promoter
CC and optionally, a heterologous nucleic acid positioned downstream from
CC the promoter and operably associated with it, where the heterologous
CC nucleic acid encodes a product disruptive of nematode attack. Also
CC claimed is a plant cell transformed with the construct making a
CC transformed plant, comprising regenerating a plant from the construct, an
CC Agrobacterium tumefaciens cell containing the construct comprising a Ti
CC plasmid, a microparticle carrying the construct, suitable for the
CC ballistic transformation of a plant cell, a plant cell protoplast
CC comprising the construct and a seed obtained from the transgenic plant.

The heterologous nucleic acid segment may be a gene encoding for an insecticidal protein, preferably a *Bacillus thuringiensis* crystal protein toxic to insects, but may be a product toxic to the plant cell. The transgenic plant is a dicot or monocot, preferably a tobacco (*Nicotiana tabacum*) plant. The construct is used for making a transgenic plant, such as a tobacco plant, that is resistant to cyst and root knot nematodes. An advantage of the invention is that two or more promoters can be easily chained to a single structural gene. The sequence presented is the N. tabacum Nicot2 protein.

SO Sequence 500 AA;

Query Match 86.5%; Score 32; DB 7; Length 500;
Best Local Similarity 85.7%; Pred. No. 5.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
|||:|
DB 228 YSSSLHS 234

RESULT 30

ABU25460
ID ABU25460 standard; protein; 277 AA.

XX ABU25460;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #10987.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Clostridium difficile.

XX WO200277183-A2.

PD 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362599P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Foretyn RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA29330.

XX Claim 25; SEQ ID NO 53384; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 623 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation and the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway

required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antitumor; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

SO Sequence 277 AA;

Query Match 83.8%; Score 31; DB 6; Length 277;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6
|||:|
DB 94 YSSNLH 99

RESULT 31
AA97205
ID AA97205 standard; protein; 347 AA.

XX AA97205;

DT 12-SEP-2003 (revised)

DT 22-DEC-2000 (first entry)

DE Campylobacter jejuni OH4384 Beta-1,4-GalNAc transferase.

XX Biosynthetic locus; biosynthesis; lipid A biosynthesis;

XX acetyltransferase; glycosyltransferase; Beta-1,4-GalNAc transferase;

XX Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase;

XX sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody;

XX immunity; immunogen; ganglioside.

XX Campylobacter jejuni; OH4384.

XX WO200046379-A1.

XX 10-AUG-2000.

XX 01-FEB-2000; 2000WO-CA000086.

XX 01-FEB-1999; 99US-0118213P.

XX 31-JUN-2000; 2000US-00495406.

XX (CANA) NAT RES COUNCIL CANADA.

XX Gilbert M, Makarchuk WW;

XX WPI; 2000-524418/47.

XX N-PSDB; AA53722, AA53720.

XX Novel glycosyltransferase polypeptides and polynucleotides useful for reagents and as immunogen for producing antibodies.

XX Claim 13; Page 100-101; 120pp; English.

A reaction mixture for the synthesis of a sialylated oligosaccharide is

CC useful for synthesizing sialylated oligosaccharide such as ganglioside,
CC lysoganglioside or their mimics. Glycosyltransferases are useful for
CC chemo-enzymatic synthesis of oligosaccharides, including gangliosides and
CC other oligosaccharides that have biological activity. The enzymes and
CC nucleic acids that encode them are useful for studies of the pathogenesis
CC mechanisms of organisms that synthesize ganglioside mimics, such as *C.*
CC jejuni and the nucleic acids are used as probes to study expression of
CC genes involved in ganglioside mimetic synthesis. Antibodies raised
CC against the glycosyltransferases are also useful for analyzing the
CC expression patterns of these genes involved in pathogenesis. The nucleic
CC acids are also useful for designing antisense oligonucleotides for
CC inhibiting expression of the Campylobacter enzymes that are involved in
CC the biosynthesis of ganglioside mimics that can mask the pathogens from
CC the host's immune system. The oligosaccharides are useful as diagnosing
CC reagents or as therapeutics and as immunogens for producing antibodies.
CC Bacterial glycosyltransferase can be used to catalyze the formation of
CC oligosaccharides that are identical to the corresponding mammalian
CC structures and are easier and less expensive to produce in large
CC quantity, compared to the mammalian glycosyltransferase. The bacterial
CC origin of the enzymes facilitates expression of large quantities of the
CC enzymes using relatively inexpensive prokaryotic expression systems.
CC (Updated on 12-SEP-2003 to standardise OS field)

SQ Sequence 347 AA;

Query Match 83.8%; Score 31; DB 3; Length 347;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
DB 268 FSSNHS 274

RESULT 32

ID ABJ18486 standard; protein; 347 AA.

AC ABJ18486;

DT 07-FEB-2003 (first entry)

DE Campylobacter jejuni bifunctional sialtransferase cactII #7.

XX Enzyme; gene therapy; acyltransferase; glycosyltransferase;

XX GalNAc transferase; N-Acetylglactosamine transferase;

XX Galactosyltransferase; sialyltransferase; sialic acid synthase;

XX Cytidine 5'-monophosphate sialic acid synthetase;

XX CMP sialic acid synthetase; acetyltransferase; ganglioside synthesis;

XX ganglioside mimetics; inflammation; tumour metastasis.

XX Campylobacter jejuni.

XX MO200274942-A2.

XX 26-SEP-2002.

XX 22-FEB-2002; 2002WO-CA000229.

XX 21-MAR-2001; 2001US-00816028.

XX (CANADA) NAT RES COUNCIL CANADA.

XX Gilbert M, Wakarchuk MW;

XX WPI; 2003-040554/03.

XX N-PSDB; ABT13673.

XX New glycosyltransferases from Campylobacter, useful for synthesizing

XX gangliosides and ganglioside mimetics, and in studying the pathogenesis

XX mechanisms of organisms that synthesize ganglioside mimetics.

XX The invention comprises the amino acid and coding sequences of
CC Campylobacter jejuni proteins. The *C. jejuni* proteins of the invention
CC may be either an: acyltransferase; glycosyltransferase; GalNAc (N-
CC Acetylglactosamine) transferase; galactosyltransferase;
CC sialyltransferase; sialic acid synthase; cytidine 5'-monophosphate (CMP)
CC sialic acid synthetase; acetyltransferase. The *C. jejuni* DNA and protein
CC sequences of the invention are useful for ganglioside synthesis, studying
CC ganglioside mimetics, and for designing oligonucleotides to inhibit
CC expression of Campylobacter enzymes involved in the biosynthesis of
CC ganglioside mimetics that can mask the pathogen's from the host's immune
CC system. The *C. jejuni* oligosaccharides of the invention may be used as
CC diagnostic reagents (e.g. to locate areas of inflammation or tumour
CC metastasis). The present amino acid sequence represents a Campylobacter
CC jejuni protein of the invention

SQ Sequence 347 AA;

Query Match 83.8%; Score 31; DB 6; Length 347;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
DB 268 FSSNHS 274

RESULT 33

ID ABP80364 standard; protein; 380 AA.

AC ABP80364;

DT 07-MAR-2003 (first entry)

DE N. gonorrhoeae amino acid sequence SEQ ID 7258.

XX Antibacterial; infection; vaccine; gene therapy.

XX Neisseria gonorrhoeae.

XX MO200279243-A2.

XX 10-OCT-2002.

XX 12-FEB-2002; 2002WO-IB002069.

XX 12-FEB-2001; 2001GB-00003424.

XX (CHIR-) CHIRON SPA.

XX Fontana MR, Pizza M, Maignani V, Monaci E;

XX WPI; 2003-058415/05.

XX N-PSDB; ABZ41334.

XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a

XX medicament for treating or preventing N. gonorrhoeae infection.

XX Disclosure; Page 716; 815pp; English.

XX The present invention relates to proteins from Neisseria gonorrhoeae.

XX Also disclosed are the nucleic acid molecules encoding the proteins and

XX antibodies that specifically bind to the proteins. The composition

XX comprising the protein, nucleic acid or antibody is useful for the

XX manufacture of a medicament for treating or preventing N. gonorrhoeae

XX infection, this may be in the form of a vaccine or gene therapy.

XX Sequences given in records ABP76736-ABP81046 represent nucleic acid

XX molecules of the invention

SQ Sequence 380 AA;

Query Match 83.8%; Score 31; DB 6; Length 380;

Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 48 YANLHS 54

RESULT 34
AAM97437
ID AAM97437 standard; peptide; 14 AA.

AC AAM97437;

DT 24-JAN-2002 (first entry)

DE Human peptide #712 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cyostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; cholestase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US035498.

PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.

PS Disclosure; Page 3823; 4143pp; English.

XX The present invention relates to oligonucleotides (see AU26793-AU34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC protein, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and cholestases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms

XX Sequence 14 AA;

Query Match 81.1%; Score 30; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLHS 7
DB 2 SSNLHS 7

RESULT 35
ABO12747
ID ABO12747 standard; peptide; 23 AA.

AC ABO12747;

DT 25-AUG-2003 (first entry)

DE Human zinc finger DNA binding domain #1046.

XX Composite binding polypeptide; zinc finger nucleic acid binding domain;
KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;
KW human.

OS Homo sapiens.

PN WO200299084-A2.

PD 12-DEC-2002.

PF 04-APR-2002; 2002WO-US022272.

PR 04-APR-2001; 2001GB-00008491.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Moore M, Sepp A, Isalan M, Choo Y;

DR WPI; 2003-278214/27.

PT New composite binding zinc finger polypeptide, useful for designing
PT sequence-specific binding proteins regulating gene expression in the
PT fields of molecular biology, and for the diagnosis and treatment of
PT autoimmune disorders.

PS Example 2; Page 93; 157pp; English.

XX The invention relates to a composite binding polypeptide comprising a
CC first natural binding domain derived from a first natural binding
CC polypeptide and a second natural binding domain derived from a second
CC natural binding polypeptide, where the first and second natural binding
CC polypeptides may be the same or different and where the polypeptide binds
CC to a target differing from the natural target of both the first and
CC second binding polypeptides. The invention also relates to a chimeric
CC polypeptide comprising a binding polypeptide cited above and a biological
CC effector domain, a library of natural binding domains, a library of
CC natural zinc finger nucleic acid binding domains comprising a linker
CC attached to it, a method for selecting a binding polypeptide capable of
CC binding to a target site and a method for designing a composite binding
CC polypeptide. The methods and compositions of the present invention are
CC useful for designing sequence-specific binding proteins for regulation of
CC gene expression in the fields of molecular biology. They can also be used
CC for the diagnosis and treatment of autoimmune disorders, and as research
CC tools and in transgenic animals. This sequence represents a human zinc
CC finger DNA binding domain used in the scope of the invention

XX Sequence 23 AA;

Query Match 81.1%; Score 30; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLHS 7
DB 13 SSNLHS 18

RESULT 36

ABP03340
ID ABP03340 standard; protein; 56 AA.
XX
AC ABP03340;
XX
DT 24-JUN-2002 (first entry)
DE Human ORFX protein sequence SEQ ID NO:6662.
XX
XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KM hyperproliferative disorder; psoriasis; benign tumor; haemorrhage;
KM degenerative disorder; osteoarthritis; neurodegenerative disorder;
KM cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KM hypertension; hypothyroidism; cholesterol ester storage disease;
KM immune deficiency; immune disorder; infectious disease;
KM autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KM myasthenia gravis.
XX
OS Homo sapiens.
XX
PN MO200192523-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001MO-US010836.
XX
PR 30-MAY-2000; 2000US-0206132P.
PR 29-AUG-2000; 2000US-0228716P.
XX
PA (CURA-) CURAGEN CORP.
PI Shimkete RA, Leach MD;
XX
XX N-PSDB; ABN19092.
DR
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
XX
PS Disclosure; SEQ ID NO 6662; 1037bp; English.
XX
XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP1500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ
XX
XX Sequence 56 AA;

Query Match 81.1%; Score 30; DB 5; Length 56;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGSNLS 7
Db 17 YSSHIS 23
RESULT 37
AAU59057
ID AAU59057 standard; protein; 83 AA.
XX
XX AAU59057;
XX
DT 13-FEB-2002 (first entry)
DE Propionibacterium acnes immunogenic protein #19953.
XX
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
KM uveitis; endophthalmitis; bone joint; central nervous system; ELISA;
KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KM dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
OS
XX
PN MO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001MO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX N-PSDB; AAS59597.
DR
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 20252; 1069bp; English.
PS
XX Sequences AAU9105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and to
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence. For example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ
XX
XX Sequence 83 AA;

Query Match 81.1%; Score 30; DB 4; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;